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GenCore version 5.1.6
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OM nucleic - nu	- nucleic search, using sw model
Run on:	April 26, 2005, 06:16:24 ; Search time 3121 Seconds (without alignments) 7207.941 Million cell updates/sec
Title: Perfect score: Semence:	US-10-069-386A-1 591 1 atggaggggttgaagag

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: EST:*

Be: BST:*

1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
9: gb_gss1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES	Ω			CN304584	30	0518	60124	34	459	35	459	8680	953	2018	228	630		51	54	BG105954	5	548	37	CN304593	
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ALIGNMENTS

AV408336	
	AY408336 591 bp DNA linear GSS 12-DEC-2003
DEFINITION H	piens HCM3190 gene, VIRTUAL TRANSCRIPT, parti
	ice.
NO	AY408336
VERSION	AY408336.1 GI:39764307
DS	GSS.
ORGANISM H	Bu
ш	, Metazoa; Chordata;
	ammalia; Euth
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AUTHURS	•
- 0	Toda, M.A., Tanenbaum, D.M., CIVELLO, D.K., Lu, F., Murphy, B., Borrions C. Wang C. Thong Y H. White T. I. Shingky, I.I.
44	•
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED 1	
	2 (bases 1 to 591)
AUTHORS	
F	, Tanenbaum, D.M., Civello, D.1
124	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
	χ. Ο.
	bmission
JOURNAL	
	ille, MD 20850, USA
COMMENT	
	them based on alignment.
FEATURES	ŏ
Bource	1591
	/organism="Homo Bapiens"
	/db_xrer="taxon:9606"
gene	<1>591 /1
MISTOC	/ TOCUS_tag="HCM3190"
ORIGIN	
/ Match	99.7%; Score 589.
Matches 59	n similarity 99.8%; Freq. No. 1.08-135; 590: Conservative 0: Mismatches 1: Indels 0: Gabs 0:

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1 (bases 1 to 729)

3 Libases 1 to 729)

4 Libases 1 to 729)

5 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.

6 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,

7 Lebkowski, J and Stanton, L.W.

7 Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

8 Nat. Biotechnol. 22 (6), 707-716 (2004)

8 Contact: Brandenberger R

8 Regenerative Medicine

9 Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

7 Tel: 650 473 7760

8 Fax: 650 473 7760
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17000600512783 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequ CN304585
CN304585.1 GI:47320999
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                                             CCCCTCTTCCTGGGCGAGGATTTCTCCCTGTCAGCCACCATTGGCTCTATC
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/mol_type="mRNA"
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mitogen-treated hES cell line H7"
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from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks tha
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
                                                                                                                                                                                                                         CCCCTCTTCCTGGGCGAGGATTTCTCCCTGTCAGCCACCATTGGCTCTATCCTCAGG
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Pred. No. 1.7e-135;
; Mismatches 1;
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Mammalia; Eutheria; P
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11 Similarity 99.8%
590; Conservative
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1. .1038
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
     E 1 (bases 1 to 1038)

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12766 row: i column: 08
High quality sequence start: 32
High quality sequence stop: 703.
Location/Qualifiers

Location/Qualifiers
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Pred. No. 1.8e-135;
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db_xref="taxon:9606"

tissue_type="embryonic"
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Fax: 650 473 7760

Email: rbrandenberger@geron.com
Insert Length: 742 Std Error:
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2 (bases 1 to 1298)
Genoscope.

Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr.
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                           Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ012YJ05"
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Genoscope.

Direct Submission

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 1318)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Pred. No. 1.9e-135;
; Mismatches 1;
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CS0DI057YM14 of
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI057YM14"

/tissue_type="Placenta Cot

/plasmid="pcMVSPORT_6"
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CR601245.1 GI:504820
HTC; CNSLT cDNA.
Homo sapiens (human)
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il Similarity 99.8%;
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full-length cDNA
of Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 646)

S Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,

Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,

Lebkowski, J and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA
Rubin (University synthesis kit Technologies).
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                                                                             Length
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                                                                             Score 582.6; DB 5;
Pred. No. 8.8e-134;
); Mismatches 6;
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Homo sapiens
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Best Local Similarity
Matches 585; Conser
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5952523"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: adaptor: GGCACGAG(G). Library constructed by
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AGENCOURT_6925371 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5957, mRNA sequence.

BU157342

BU157342.1 GI:22670874

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1056)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2140 row: k column: 20
High quality sequence stop: 587.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   TGGGAGTGGAATGAACTGGATCACATCATGGAAATCATTCTGGGGTCCTAA 591
 AAGGAGCCTGCACGGGCCCCACAGAGCCTCCTCACAACCTCTTCTGTGCCCCA
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Matches 588; Conservative
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                                                                                     /tissue_type="embryonic stem cell, retinoic acid mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/note="oligo dT_primed, full-length enriched cDI from hES cell line H7 (p29) maintained in feeder conditions. Embryoid bodies were generated in the of all-trans retinoic and mitogens."
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BX398356 Homo sapiens PLACENTA COT 25-NORMALIZED Homo clone CS0DI057YM14 5-PRIME, mRNA sequence.
BX398356
BX398356.2 GI:46846521
EST.
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                                                                                                                                                                           Score 580.4; DB 7;
Pred. No. 2.8e-133;
0; Mismatches 1;
                               00.
                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 646 Std Error:
Location/Qualifiers
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                                                                                                                                                                            98.2%;
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Best Local Similarity 99.8
Matches 581; Conservative
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(human)

Homo sapiens Homo sapiens

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1017)

5 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30613656.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Location/Qualifiers
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Pred. No. 4.3e-132;
); Mismatches 2;
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Homo sapiens (human)

SM Homo sapiens

Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia; Eutheria, Primates, Catarrhini; Hominidae, Homo.

B 1 (bases 1 to 873)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14061 row: e column: 20

High quality sequence stop: 605.

Location/Qualifiers
                                                                                                                                                                                                                                                                      873 bp mRNA linear EST 12-SEP-2002
5', mRNA sequence.
BU508982.1 GI:22815215
EST.
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1
Site_2: Sall; Cloned unidirectionally. Primer: Oligo d'Average insert size 2.1 kb. "
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Pred. No. 4e-130;
0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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nilarity 98.5%;
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                          Euteleostomi
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodie derived_from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT_primed, full-length enriched cDNA from embryoid body outgrowths derived from hES cel H1 (p32), H7 (p29), and H9 (p26) maintained in fee conditions."
                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 712)
mRNA sequence
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Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025,
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 712 Std Brror: 0.00.
                                                                                                         CN304594 712 bp mRNA 1
17000532611443 GRN_EB Homo sapiens cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 575.2; DB 7;
Pred. No. 5.6e-132;
0; Mismatches 3;
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                                                                                                                                                         GI:47321008
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Best Local Similarity 99.3%;
Matches 588; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cmagness@illumigen.com
Sequenced on 2004.07.15. 648 Q20 bases. Library Preparation:
Michael Katze Lab at University of Washington DNA Sequencing
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
                                                                                                                                                                                                                                                                                                               770
                                                                                                                                                                                                                                                                                                                                                                   ILLUMIGEN MCQ_49981 Katze_MMIL Macaca mulatta cDNA clone IBIUW:19438 5' similar to Bases 114 to 970 highly similar CO579535 (Hs.169138), mRNA sequence.
CO579535 GI:50410495
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (rhesus monkey)
Macaca mulatta
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae
Cercopithecinae; Macaca.

1 (bases 1 to 970)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnes
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
                                            CCCCTCTTCCTGGGCGAGGATTTCTCCCCTGTCAGCCACCATTGGCTCTATC
                                                                                                                                             CTCCAGAATGAAGTGCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGC
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ACCCTCCAACAGCTGCAGCTGCACTTCGCCTGGCTCCCGCCCCTGCCCTGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, S
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:19438"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
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ol type="mRNA"
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Brownstein (NHGRI),
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Catarrhini, Hominidae,
                                                                                   Length
                                                                                                        Indels
/dev_stage="adult"
/lab_host="Electromax DH10B"
/clone_lib="Katze_MMIL"
/note="Organ: ileum; Vector: pDONR 222;
Site_2: BsrG I; Created from CloneMiner
Construction kit (catalog #18249-029)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene
                                                                                  Score 560.8; DB 7;
Pred. No. 2.2e-128;
); Mismatches 12;
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Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668 bp mRNA
Homo sapiens cDNA
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Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrhir
1 (bases 1 to 668)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalia
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M
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RESULT 14
BX362283
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SOURCE
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                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4824464"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLM
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10736 row: a column: 09
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Pred. No. 3.7e-128;
0; Mismatches 3;
                                                                              Plate: LLAM10736 row: a column: 09
High quality sequence stop: 666.
Location/Qualifiers
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Best Local Similarity 99.5%;
Matches 561; Conservative
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Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1001 bp mRNA linear EST 08-APR-2004 CELLS (JURKAT CELL LINE) COT 10-NORMALIZED CS0DJ012YJ05 5-PRIME, mRNA sequence.
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                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1001)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370588.

Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JURKAT CELL LINE) COT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DJ012CE03QP1&c=9131.r Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone_lib="Homo sapiens T CELLS (JURKAT)
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Pred. No. 1.1e-127;
1; Mismatches 2;
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                  BX362283 Homo sapiens T
Homo sapiens CDNA clone
BX362283
BX362283.2 GI:46289607
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il Similarity 99.1%;
581; Conservative
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Homo sapiens
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Matches 58
                      DEFINITION
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AUTHORS
TITLE
JOURNAL
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/clone="IMAGE:5722856"
/lab_host="DH10B"
/clone lib="NIH MGC_125"
/lone lib="NIH MGC_125"
/clone lib="NIH MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to site_1: brary is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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TACTTGGGGGACTCTGGCCTGGATGACTTCTTTCTGGACATTGACACTTTGCGGTAGAA
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1 (bases 1 to 1045)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MG Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12709 row: j column: 09
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Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                644 TGCGGAGTGGAATGAACTGGATCACATCATGGAAATCATTCTCGGG
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Pred. No. 2e-127;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM12709 row: j column
High quality sequence start: 20
High quality sequence stop: 626.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        GI:18779156
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ilarity 98.6%;
Conservative C
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5', mRNA sequence
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Homo sapiens
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582; Conser
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BM546306
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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KEYWORDS
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CTCCAGAATGAAGTGCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCGG
                                                                                                                           TACTTGGGGGACTCTGGCTTGACTTCTTTCTGGACATTGACATCTGCGGTAGAA
                ccccrcrrcraggcgaggarrrcrccrgrcagccaccarrggcrcrargg
                                                                                28
                                                                                                                                                                      2005, 10:11:1
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cch completed: April time : 3125 secs

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us-10-069-386a-2

5.1.6 Compugen Ltd version - 2005 GenCore (c) 1993 Copyright

mode1 BK protein search, using OM protein Search time 166 Seconds (without alignments) 456.657 Million cell upo •• 12:21:55 2005, 25, April Run on:

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196

... APGSWEWNELDHIMEIILGS

US-10-069-386A-2 1033 1 MEGGLKRKHSDLEEEEERWE.... score Title: Perfect

Gapext BLOSUM62 Gapop 10.0 Scoring table:

Sequence:

386760381 residues 2105692 seqs, Searched:

0.5

2105692 hits satisfying chosen parameters: of Total number

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

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A_Geneseq_16Dec04:* Database

geneseqp1980s:*
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No score gand is

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ALIGNMENTS

RBT1; replication protein A binding transcriptional activator 1; RPA32; gene therapy; apoptosis; cancer; leukaemia. Replication protein A binding transcriptional activator 1 RBT1 Æ standard; protein; 196 (first entry) 23-MAY-2001 AAB35402; AAB35402 RESULT 1

Unidentified

WO200114546-A2

01-MAR-2001.

2000WO-CA000948. .17-AUG-2000; 99US-0149472P. 19-AUG-1999;

TRANSLATIONAL RES IN CANCER (TRAN-) CENT

Cho JM; Alaoui-Jamali MA,

2001-218447/22 WPI;

N-PSDB; AAF28052

Novel replication protein A binding transcriptional activator 1 gene, useful for treating neoplastic disorders such as cancer and in gene therapy.

Disclosure; Fig 1; 16pp; English

The present invention provides the protein and coding sequences of the replication protein A binding transcriptional activator 1 (RBT1). The protein is capable of inducing apoptosis. The sequences are useful in the gene therapy and other methods of treatment of cancer, including leukaemias. The present sequence is the RBT1 protein

Sequence 196 AA;

ö Gaps ö 196; Length Indels Query Match
Best Local Similarity 100.0%; Score 1033; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 196; Conservative 0; Mismatches 0;

MEGGLKRKHSDLEEEEERWEWSPAGLQSYQQALLRISLDKVQRSLGPRAPSLRRHVLIHN

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Homo
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T, Koga
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3, Otsuki
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K, Kojima
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larity 99.5%;
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11-JAN-2000;
02-MAY-2000;
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T, Koga
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K, Kojima
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th human cDNAs.
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Matches 195; Conservative
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N-PSDB; ADL32051.
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P cancers used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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                                                                                                                                                                                                                                                                                                                                                                                                  Human; colon cancer; colorectal carcinoma.
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03-NOV-1999;
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a wector comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of methods of selling and/or licensing single exon probes or microarrays to
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                                                                                                                              SATIGSILRELD
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                                                                         SIGPRAPSLRRHVLIHNTLQQLQAALRLAPALPPRPLFLGEEDFSL
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Score 791; DB 4; Le
Pred. No. 5.4e-69;
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                                                                                                                                                                                                                                                                                                                                                                                    exon protein #6309
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                                                                                                                                                                                                          ARAPPEPXHNLFCAPGSWEWNELDHIMEIILGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 33709; 80pp; English.
                                                                                                                                                                                                                                                                                              ABO60075 standard; protein; 142 AA
                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002US-00029386.
            76.6%;
ilarity 98.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                    derived single
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-119264/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR,
                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissues.
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                                                                                                                                                                                                                                                                                                                                                                                      Human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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                                         150;
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                                                                                                                                                                                                                                                                                                                           ABO60075;
             Query Match
Best Local S
Matches 150
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ABO6007
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a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                        1,
                                                                                                                                                                                               is a human
                                                                                                                                                                                                                                                                                                                                                                                      130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELDHIM
                                                                                                                                                                                                                                                                                                                                                                                      VPPQPD
                                                                                                                                                                                                                                                                                                                                                                                                      18 LPPLPC-PPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPONPVTPLGLONEVPPOPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVFLEALSSRYLGDSGLDDFFLDIDTSAVEKEPARAPPEPPHNLFCAPGSWEWNELDHIM
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 PVFLEALSSRYLGDSGLDDFFLDIDTSAVEKEPARAPPEPPHNLFCAPGSWEWN
                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                         Length 142;
                                                                                                                                                                                                                                                                                                                                                                                      LAPAPALPPEPLFIGEEDFSLSATIGSILRELDTSMDGTEPPQNPVTPL
                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                         DB 8;
                                                                                                                                                                                                                                                                                                                      Score 645.5; DB 8;
Pred. No. 7.8e-55;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon protein #6308
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96.8%;
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RANK D R.
HANZEL D K.
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                                                                                                                                                                                                                                                                                                                                     l Similarity
122; Conser
                                                                                                                                                                                                                                                                                          Sequence 142 AA;
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
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(RANK/)
(HANZ/)
                                                                                                                                                                                                                                                                                                                                                      Matches
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ABO60074
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 6888 amino acid sequences conductions to a nucleic acid molecule expressed in human calls or tissues. Also included are a spatially-defined in the specification. The probe is a single exon probe that human calls or tissues. Also included are a spatially-defined and human calls or tissues. Also included are a spatially-defined and probes cited above, where each of the plurality of probes is separately probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a vector comprising at least 8 configuous amino acids of any of the above- mentioned amino acid sortionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to contiguous amino acids of any of the above- methods of providing human gene expression data by subscription, and a computer-readable exon probe cited above. The probes methods and actabases having a plurality of records to caute or for the probes methods and actabases having a plurality of records cited above. The probes may be used as tools for surveying tissues to detect the presence of expression of a single exon probe cited above. The probes may be used as tools for surveying alternative splicing events, in detecting and characterising alternative splicing events, in detecting and characterising a laternations in the genomic locus that includes their exon, in assessing alternative splicing events, in detecting and characterising general expression of a single exon probe protein of the invention. Where The sequence is a human strip patent did not form part of the present especial carids.

Single 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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Mismatches 9;
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80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 402;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLOQLQAALRLAPAPALPPEPLFLGEEDF
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Similarity 89.9%;
0; Conservative
SEQ ID NO 33708;
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Claim 45;
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10-JUN-2004.
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Best Local
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Matches
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                                                                                                                                                                                                   This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152
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                                                                                                                                                                                                                                                                                                                                                                      Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                             Edwards
                                                                                                                                                                                                                                                                                                                                                                     Score 216; DB 2;
Pred. No. 1.4e-12;
36; Mismatches 69
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                                                                                                             Milne
                                                                                                                                                                                   516pp; English
                                                                                                                                                              New isolated human secreted proteins
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98US-0074121P.
98US-0081563P.
98US-0096116P.
                     98WO-IB002122
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                                                                                                                                                                                   330-331;
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                                                                                                                                1999-385906/32
)B; AAX97688.
                                                                                                                                                                                                                                                                                                                                                                               Similarity 76; Conser
                                                                                                                                                                                                                                                                                                                                                   Sequence 236 AA;
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                                                                                         GENSET
                                                                                                            Bougueleret L,
                                                                                                                                                                                  9; Page
                                      17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
                    17-DEC-1998;
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The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the collypeptide to an antibody. The polynucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing between human tissues and cells, and for distinguishing between human tissues and cells, and for the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
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larity 32.6%; Pred. No. 1.46
Conservative 36; Mismatches
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99WO-IB000282.
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2000US-00663600.
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09-FEB-1999;
21-JUN-2000;
15-SEP-2000;
15-OCT-2001;
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CECRP-3; cell cycle regulation protein-3; cell profits cirrhosis; cell proliferative disease; cancer; atherosclerosis; cirrhosis; hepatitis; psoriasis; immune system disorder; allergy; asthma; acquired immune deficiency syndrome; Crohn's disease; Blast methrheumatoid arthritis; gene therapy; chromosomal mapping.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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-WNELDHIMEIILGS
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K, Kojima
- PARAPPEP - PHNLFCAPGSWE
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2000JP-00118774
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Best Local Similarity
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N-PSDB; AAK94674.
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11-JAN-2000;
02-MAY-2000;
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Query Match

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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
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larity 32.6%; Pred. No. 2.7e-12;
Conservative 36; Mismatches 69
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                                                                                                                  DIDTSAVEKE - - - PARAPPEP - PHNLFCAPGSWE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K,
K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3677; 1340pp; English
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                                                  LDTSMDGTEPPQNPVTPLGLQNEVPP-
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Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                      236
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2000JP-00118774.
2000JP-00183865.
2000EP-00114089.
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                                                                                                                                                                                                                                      standard; protein;
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L-SHIEGLSQAPQP
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N-PSDB; ADL31643.
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nes 76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length human cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 236 AA;
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                                                                                                                                                                                                                                                                                                                                        Human protein
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11-JAN-2000;
02-MAY-2000;
07-JUL-2000;
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Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1396543-A2
                                                                                                                                                                                                                                                                                                       20-MAY-2004
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                                                                                                                                                                                                                                                                      ADL31644;
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Matches
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used as DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                       gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine whi patients may be in need of restorative therapy. The GENSET polypeptic may be used as antigens in the production of antibodies and in assays identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted
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                                    Full length GENSET human nucleic acids encoding potentially proteins, useful in gene therapy and vaccination against a diseases, and for diagnosis of those diseases.
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larity 32.6%; Pred. No. 2.7e-12.
Conservative 36; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jobert
                     DIDTSAVEKE---PARAPPEP-PHNLFCAPGSWE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 889-890; 921pp; English
                                                                                                                                                                                                                                       ID NO: 412
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2000US-0187470P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENSET
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06-MAR-2000;
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                                                                                                                                                                       AAG89292;
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Best Local (
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                                    152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        static;
nfection;
ammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       anaemia;
                                                                                                                                                                                                                                                                                                                                                                                Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

antinflammatory; antirheumatic; antiarthritic; immunosuppressive;

antibacterial; endocrine; cardiant; central nervous system; virucide;

anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia

misagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;

dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

meuroprotective; antidepressant; nootropic; antiparkinsonian; infectio

meuroprotective; antidepressant; nootropic; antiparkinsonian; inflammatio

meuroprotective; rheumatoid arthritis; septic shock; pancreatitis;

antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity

genetic disease; haematopoietic disorder; platelet disorder; asthma;

thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

allergic rhinitis; diabetes; multiple sclerosis; depression;

neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eczema;
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LEGLFE
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64 LRHLVLVVVNTLRRIQAS--MAPAALPPVPSPPAAPSVADNLLASSDAALSASM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding polypeptides, useful for cancer, ulcers and HIV infection
                                     -OPDPVFLEAL -- SSRYLGDSG
                                                                        ---LADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDG
                                                                                                           Isolated human polynucleotides encoding treatment and diagnosis of e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:1065.
                                    LDTSMDGTEPPQNPVTPLGLQNEVPP-
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                                                                      L-SHIEGLSQAPOP-
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21-JAN-2000;
25-APR-2000;
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              inflammation,
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of disorders associated with the activity of a protein e.g. inflammatic rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders
                                                                                                                                                                                                                                                       -LLRISLDKVQRSLGPRAPS
                                                                                                                                                                                                                                                                                                           L-SHIEGLSQAPQP----LADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFE
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                                                                                                                                                                                                                                                                                                                                                   -OPDPVFLEAL--SSRYLGDSGLDDFFL
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                                                                                                                                                                                                                                                                                                                                                                                                                      DIDTSAVEKE----PARAPPEP-PHNLFCAPGSWE-----WNELDHIMEIILGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; vaccine;
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this residue"
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residue"
                                                                                                                                                                                   25.0
                                                                                                                                                                                Score 213; DB 4
Pred. No. 3.4e-1;
; Mismatches
                                                                                                                                                                                                                                       -ERWEWSPAGLQSYQQA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g21_1; human; therapy;
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this residue
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                                                                                                                                                                               th 20.6%; Similarity 32.6%; 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein;
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                                                                                                                                                                           AAY31828-38) and polynucleotides (see AAZ19893-901) isolated from foetal cell, adult blood cDNA clone (see AAX19894). The invention provides new human secreted proteins (see AAX19894). The invention provides new human secreted proteins (see AAX18828-38) and polynucleotides (see AAZ19893-901) isolated from foetal cell, adult blood, adult brain and foetal kidney cDNA libraries. They are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data are given. Suggested activities include nutritional, cytokine, tissue growth, cell proliferation and differentiation, immunostimulant (e.g. as vaccine), immunosuppressive, haemostatic or thrombolytic, receptor/ligand activity, antiinflammatory, cadherin or tumour invasion suppressor, and tumour inhibition activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LAXEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFE
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                                                                      Evans
                                                                                                                                                                                                                                                                                                                            Length 236;
                                                                                                                                                                      of a novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression; single exon probe; microarray; splicing event; genomic alteration.
                                                                    Collins-Racie LA,
Steininger RJ;
                                                                                                                          cell
                                                                                                                                                                                                                                                                                                                                              70;
                                                                                                                                                                                                                                                                                                                           ; DB 2;
4.3e-12;
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                                                                                                                          fetal
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                                                                                                                                                                                                                                                                                                                                                                - ERWEWSPAGLOSYOOA
                                                                                                                                                                     acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                    LRRHVLIHNTLQQLQAALRLAPAPALPPEPL-
                                                                                                                          derived from murine
                                                                                                                                                                                                                                                                                                                             Score 211;
Pred. No. 4
                                                                                                                                                    Claim 13(a); Page 94; 107pp; English
                                                                              Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                      LDTSMDGTEPPQNPVTPLGLQNEVPP
                                                                                                                                   vaccines
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99US-00078803
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                                                                                                                         polymucleotides
                                                                                             WPI; 1999-562059/47
N-PSDB; AAZ19894.
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                                                                      Mccoy
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17-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene
alternative
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Matches 76
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                                                   (GEMY)
                                                                      Jacobs
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridies under high stringency conditions to a nucleic acid molecule expressed in human cells or issues. Also included are a spatially-addressable set of single exon nucleic acid molecule probes cited above, where each of the plurality of probes is separately addressably isolateable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a wettor comprising the single exon microarray for measuring human gene expression, a vector comprising the single exon microarray for measuring human gene expression, a method of providing contiguous amino acids of any of the above- mentioned amino acid solated and/or licensing single exon probes or microarrays to solated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays or acustomer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records cited above. The probes methods and apparatus are useful in gene cited above. The probes may be used as tools for surveying tisquest to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays alterations in the genomic alterations, in priming the synthesis of nucleic acide, or in expressing the ORF-encoded peptide or the species of the probes are useful in general exon probe grower and in detecting and characterising grower alternative splicing events, in detecting and characterising sor in expressing the ORF-encoded peptide or the synthesing the probes are use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                         New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ERWEWSPAGLOSYQOA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 34001; 80pp; English.
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illarity 32.6%;
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                                                                                                                      2002US-00029386
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(RANK/) RANK D R.
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                                                    03-APR-2002;
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16-OCT-2003
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Search completed: April 25, 2005, 12:29:28 Job time : 170 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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OM protein - protein search, using sw model

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196

US-10-069-386A-2 1033 1 MEGGLKRKHSDLEEEERWE.....APGSWEWNELDHIMEIILGS Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

residues 283416 segs, 96216763 Searched:

283416 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		* Query			SUMMARIES	
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	84	•	289	N	7045	leucine-tRNA ligas
		•	S	7	I61714	Ð
		•	1015	7	C20	phogrin precursor

RESULT 2
T40514
Chaperonin hsp78p - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C;Accession: T40514

171 -PHNLFCAPGSWEWNEL 186

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| :| | | :: 321 SPPSL--QDAEWYWGDI

335

hypothetical pro	netical p	hetical	thetical prot	able AMP-bin	robable oxidore	le ox	ypothetical prot	NA-bindin	in - in	ural pr	n-tyrosine	HC class III hi		ass III his	tailless (tll) pro
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ALIGNMENTS

	RESULT 1	
	H59435	
	phosphoin	phosphoinositide-3-kinase regulatory beta chain [imported] - human
	C;Species	C; Species: Homo sapiens (man)
	C;Date: 0)3-Jun-2002
	C; Accessi	A59436
	R;Volinia	ı S; Patracchini P; Otsu M; Hiles I; Gout I; Calzolari E; Bernardi F; Rooke L; We
	Oncogene	1992
	A; Title:	A; Title: Chromosomal localization of human p85 alpha, a subunit of phosphatidylinositol
	A; Reteren	A; Reference number: H59435
	A; Accessi	A; Accession: H59435
	A; Status:	preliminary
	A; Molecul	A; Molecule type: DNA
	A;Residue	ss: 1-728 <vol></vol>
	A; Cross-r	A; Cross-references: UNIPROT: 000459; GB: NP_005018; PID: 94826908; PIDN: NP_005018.1
	R;Janssen	1, J.W.; Schleithoff, L.; Bartram, C.R.; Schulz, A.S.
	Oncogene	
_	A; Title:	A; Title: An oncogenic fusion product of the phosphatidylinositol 3-kinase p85beta subunit
	A;Referen	ıce number: A59436; MUID:98241181; PMID:9582025
_	A;Accession	A;Accession: A59436
_	A;Status:	A;Status: preliminary
	A; Molecul	A; Molecule type: DNA
	A;Residue	
	A;Cross-r	NP_005018;
	Query Match	
	Best Local	cal Similarity 23.9%; Pred. No. 1;
	Matches	47;
	ò	20 EWSPAGLOSYQOALLAISLDKVORSLGPRAPSLRRHVLIH 59
	qo	164 QWDTAALADGIKSFLLALPAPLVTPEASAEARRALREAAGPVGPALEPPTLPLHRALTLR 223
	ò	60 NTLQQLQAALRLAPAPALPPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPQNPVTPL 119
	qa	224 FLLQHLGRVARRAPALGPAVRALGATFGPLLLRAPPPPSSP-PPG 267
	ě	
	ò	120 GLQNEVPPQPDPVFLEALSSKYLGDSGLDDFFLDIDTSAVEKEFAKAFFEF 170
	qa	268 GAPDGSEPSPDFPALLVEKLLQEHLEEQEVAPPALPPKPPKAKPAPTVLANGG 320

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protein YLR337c
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          -LP
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                                                                           -QPPPPPPPPLFMSTTSFSPSQPP
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                                           PARALPPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPONPVTPLGL
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                                                                                                             VPPQPDPVFLEALSSRYLGDSGLDDFFLDIDTSAVEKEPARAPPEPP
                                                                                                                                -TSTTSFSPSOPPPPP
          -HHHHEI PAKDSVDN-PLNLPSDPPSSGDHVTL
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                                                                                                                                                                                                                         verprolin - yeast (Saccharomyces cerevisiae)
N;Alternate names: prolin-rich protein VRP1; protei
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1995 #sequence revision 11-Aug-1995
C;Accession: S51342; S39626; S57435
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Pred. No.
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Matches 38; Conser
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F;678-685/Region:
F;704-710/Region:
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Marziali,
                                                                                                                              SPDB
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T.H.; Dewar, K.
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                                                                                                                              GSPDB:GN00067;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86441
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Di
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; I
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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Maiti, R
          S.
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R;Gwilliam, R.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, submitted to the EMBL Data Library, September 1998
A;Reference number: Z21933
                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-803 < GWI>
A; Residues: 1-803 < GWI>
A; Cross-references: UNIPROT:074402; EMBL:AL031534; PIDN:CAA20737.1; GS
A; Experimental source: strain 972h-; cosmid c4F6
C; Genetics:
A; Gene: SPDB:SPBC4F6.17c
A; Map position: 2
C; Superfamily: endopeptidase Clp ATP-binding chain
C; Keywords: ATP; molecular chaperone; nucleotide binding; P-loop
F; 139-146/Region: nucleotide-binding motif B
F; 539-546/Region: nucleotide-binding motif B
F; 539-546/Region: nucleotide-binding motif B
F; 545/Region: nucleotide-binding motif B
F; 545/Binding site: ATP (Lys) #status predicted
F; 545/Binding site: ATP (Lys) #status predicted
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-LASFLFLGP1
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A;Cross-references: UNIPROT:Q9C6S1; GB:AE005172; NID:g11136725
C;Genetics:
A;Map position: 1
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larity 24.6%; Pred. No. 4.7;
Conservative 11; Mismatches
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A;Residues: 1-1201 <STO>
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Best Local S
Matches 53
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Best Local S
Matches 41
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I.S.Y.; Mi

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A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A; Reference number: A82035; MUID:20406833; PMID:10952301

A; Accession: A82255

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-1621 < HEI>
A; Residues: 1-1621 < HEI>
A; Residues: 1-1621 < HEI>
A; Cross-references: UNIPROT:Q9KTA5; GB:AE004181; GB:AE003852; NID:g9655454; PIDN:AAF94159

A; Experimental source: serogroup 01; strain N16961; biotype El Tor

C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimotohno, K.; Takahashi, Y.; Shimizu, N.; Gojobori, T.; Golde, D.W.; Chen, I.S.Y.; Mi Proc. Natl. Acad. Sci. U.S.A. 82, 3101-3105, 1985

Proc. Natl. Acad. Sci. U.S.A. 82, 3101-3105, 1985

A;Title: Complete nucleotide sequence of an infectious clone of human T-cell leukemia vi; A;Reference number: A94042; MuID:85216449; PMID:2582407

A;Reference number: A93044

A;Rolecule type: DNA

A;Residues: 1-433 <SHI>
A;Rolecule type: DNA

A;Residues: 1-433 <SHI>
A;Rolecule type: DNA

A;Residues: 1-433 <SHI>
A;Residues: 1-433 <SHI>
A;Rolecule type: DNA

A;Residues: 1-433 <SHI
A;Residues: 1-430 <SHI
A;Residues: 1-4
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agoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (strain N16961 serogroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-Jul-2004
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                                                                                                                APŚRALGTLRODRAERRESLOKQEAIREVDŚSEDDTDEEPENŚQATOEPRLSPHPEASHN
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                                            -DSGLDDFFLDIDTSAVEKEPARAP-PEPPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LPPEPLFLGEEDFSLSA
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H.; Dragoi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p24
                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Contains: core polyprotein
N; Contains: core protein p12; core protein p15; core protein p24
C; Species: human T-cell lymphotropic virus type 2, HTLV-2
A; Note: host Homo sapiens (man)
C; Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change C; Accession: A03944
R; Shimotohno, K.; Takahashi, Y.; Shimizu, N.; Goichous Toring Troc. Natl. Acad. Sci. Troc. Natl. Sci. Matl. Acad. Sci. Troc. Natl. Acad. Sci. Troc. Natl. Acad. Sci. Troc. Natl. Sci. Matl. Acad. Sci. Matl. Acad. Sci. Matl. 
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Bass, S.;
, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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No.
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Pred.
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                                                                                                                                                                                            LFCAPGSWEWNELD
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kinase homold
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C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C; Malden, P.D.; Cowan, N.J.
M; Nol. Cell. Biol. 13, 7625-7635, 1993
A; Title: A novel 205-kilodalton testis-specific serine/threonine protein kinase associance as novel 205-kilodalton testis-specific serine/threonine protein kinase associance as preliminary
A; Residues: 1-1734 cwAL>
A; Residues: 1-1734 cwAL>
A; Residues: 1-1734 cwAL>
A; Cross-references: UNIPROT: Q60592; GB: U02313; NID: g406057; PIDN: AAC04312.1; PID: g40600
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase homology ckIN>
F; 459-467/Region: protein kinase homology ckIN>
F; 459-467/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:S76673; NID:g243439; PIDN:AAB21130.1; L backbone (NCBIN:76673, NCBIP:76674)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.C.;
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                                                                                                                                                                                                                                                                                                                                                                     transcription factor E3 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2
C; Accession: A42029
R; Roman, C.; Matera, A.G.; Cooper, C.; Artandi, S.; Blain, S.; Ward, D.C
Mol. Cell. Biol. 12, 817-827, 1992
A; Title: mTFB3, an X-linked transcriptional activator containing basic h
A; Accession: A42029
A; Accession: A42029
A; Accession: A42029
A; MulD: 92123207; PMID: 1732746
A; Accession: A42029
A; Residues: 1-446 <ROM>
A; Residues: 1-446 <ROM>
A; Residues: 1-446 <ROM>
A; Note: sequence extracted from NCBI backbone (NCBIN: 76673, NCBIP: 76674)
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9.2%; Score 95.5; I
Best Local Similarity 27.3%; Pred. No. 1.7;
Matches 48; Conservative 24; Mismatches
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26.3%; Pred. No. 15;
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                                                                                                                  GDSGLDDFFLDIDTSAVEKEPARAPPEPP
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NID:e1542263; PIDN:CAB54442.1;
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   clone DKFZp566N1047
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y48B6A.6 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex C; Accession: T26998
R; Wall, M.
submitted to the EMBL Data Library, September 1999
A; Reference number: Z20297
A; Accession: T26998
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-716 <WIL>
A; Residues: 1-716 <WIL>
A; Experimental source: clone Y48B6A
C; Genetics:
A; Experimental source: clone Y48B6A
C; Genetics:
A; Coss-references: UNIPROT: Q9U2A6; EMBL: ALI10490; NID: A; Experimental source: clone Y48B6A
C; Genetics:
A; Coss-references: UNIPROT: Q9U2A6; EMBL: ALI10490; NID: A; Experimental source: clone Y48B6A
C; Genetics:
A; Coss-references: UNIPROT: Q9U2A6; EMBL: ALI10490; NID: A; Experimental source: clone Y48B6A
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                                                                              Score 88; DB Pred. No. 12; 6; Mismatches
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; Pred. No. 14;
29; Mismatches
    source: fetal kidney;
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ilarity 24.4%;
Conservative 20
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Similarity 25.0%;
49; Conservative 2.
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A; Experimental source:
C; Genetics:
A; Note: DKFZp566N1047.1
                                                                                                    Similarity 38; Conser
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                                                                              Query Match
Best Local S
Matches 38
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A; Buthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Accession: AG0565
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-804 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD04993.1; PID:g16501778; GSPDB:GN00176
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White, N.; Farrar
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                                                                                                                                                           -DLEQLEA--KAI
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C; Species: Homo sapiens (man)
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-200C; Accession: T42644
R; Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, November 1999
A; Reference number: Z22231
A; Accession: T42644
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Kesidues: 1-651 < AAA>
A; Cross-references: UNIPROT: Q9UF93; EMBL: AL133109
                                                                                                                                                                                                                                                                              ----GLQNEVPPQPDPVFLEA----LSSRYLGDSGLDDFFLDIDTSAVEKEPARAPPE
                                                                                                                                                                                                                                                                                                   629 EDSTQLLNEVLGEPVPEELASGLEIDQNSTELLDELLDD--LDLDDESIEATEFSVAPE
                                                                                                                      13 EEEEERWEWSPAGLQSYQQALLRISLDKVQRSLGPRAPSLRRHVLIHNTLQQLQ
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                                                                                 45
                                             Length 1621;
                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein STY0554 [imported] - Salmonella enterica C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18 C; Accession: AG0565
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, Ith, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
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                                         Score 91.5; Di
Pred. No. 20;
22; Mismatches
                                                                              22;
                                        8.9%;
ilarity 27.4%;
Conservative 22
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530 EEDDDEFDLSGAGVAGDQ-
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                                                             Similarity 49; Conser
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   A; Map position:
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C;Genetics:
A;Gene: STYO
C;Superfamil
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R;Cao, L.; Zhang, L.; Ruiz-Lozano, P.; Yang, Q.; Chien, K.R.; Graham, R.M.; Zhou, M.
J. Biol. Chem. 273, 21077-21083, 1998
A;Title: A novel putative protein-tyrosine phosphatase contains a BRO1-like domain and stakeference number: Z18004; MUID:98361981; PMID:9694860
A;Reference number: Z18004; MUID:98361981; PMID:9694860
A;Accession: T14355
A;Accession: T14355
A;Accession: T1435
A;Accession: T1435
A;Accession: T1494 < CAO>
A;Cross-references: UNIPROT:088902; EMBL:AF077000; NID:g3598973; PID:g3598974; PIDN:AAC6:A;Experimental source: brain
C;Genetics:
A;Genetics:
A
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C;Species: Thiobacillus ferrooxidans
C;Saccession: B37761
R;Berger, D.K.; Woods, D.R.; Rawlings, D.E.
J. Bacteriol. 172, 4399-4406, 1990
A;Title: Complementation of Escherichia coli sigma(54) (ntrA)-dependent formate hydroge
A;Reference number: A37761; MUID:90330545; PMID:2198257
A;Accession: B37761
A;Reference number: A37761; MUID:90330545; PMID:2198257
A;Accession: B37761
A;Residues: 1-475 < BER>
A;Residues: 1-475 < BER>
A;Residues: 1-475 < BER>
A;Cross-references: UNIPROT:P24695; GB:M58480; GB:M3831; NID:g154642; PIDN:AAA27379.1;
C;Superfamily: Pseudomonas transcription initiation
C;Keywords: DNA binding; transcription regulation
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Pred. No. 48;
9; Mismatches
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Pred. No. 12;
31; Mismatches
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Similarity 29.1%;
37; Conservative 1
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14355
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   A;Molecule type: DNA
A;Residues: 1-1676 <FIS>
A;Cross-references: UNIPROT:Q00083; GB:X82289; NID:g683499; PID:g683!
C;Genetics:
A;Gene: apsA
A;Introns: 149/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 06-Jul-1990 #sequence_revision 09-Oct-1992 #text_change
C;Accession: A34596; 310379
R;Beckmann, H.; Su, L.K.; Kadesch, T.
Genes Dev. 4, 167-179, 1990
A;Title: TFE3: a helix-loop-helix protein that activates transcr
A;Reference number: A34596; MUID:90249724; PMID:2338243
A;Reference number: A34596; MUID:90249724; PMID:2338243
A;Accession: A34596
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-536 <BEC>
A;Cross-references: UNIPROT:P19532; EMBL:X51330; NID:g37061; PID
A;Note: the authors translated the codon ACC for residue 433 as
C;Genetics:
A;Gene: GDB:TFE3
A;Cross-references: GDB:125870; OMIM:314310
A;Map position: Xp11.23-Xp11.22
C;Keywords: DNA binding; transcription factor
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residues 332791073 1424015 segs, Searched

1424015 hits satisfying chosen parameters: of Total number

Minimum DB seq Maximum DB seq

2000000000 length: length: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

Database

Published

Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

a rinted, No. is the number of results predicted by chance to have greater than or equal to the score of the result being particular derived by analysis of the total score distribution. of Pred. No. score gre and is de

SUMMARIES

		de				
Result No.	Score	Query Match	Length	DB	. QI	Description
	1 0	76.	157	14	US-10-106-698-5516	Segmence 5516. Ap
N	645.5	62.5	142	14	US-10-029-386-33709	
m	40	8	111	14	US-10-029-386-33708	Sequence 33708, A
4	$\boldsymbol{\vdash}$	0	236	11	US-09-978-360A-568	
	$\boldsymbol{\vdash}$	0	236	σ	US-09-731-872-412	412,
'	\vdash	0	236	10	US-09-876-997-412	Sequence 412, App
7	_	0	278	15	US-10-296-115-1065	106
80	0	19.8	222	14	US-10-029-386-34001	34
σι	C	3	237	13	-01	7
10	N	2	314	15	US-10-170-385-31	Sequence 31, Appl
11	N		314	16	US-10-755-889-627	62
12	106	10.3	254	σ	US-09-925-302-596	969
13	106	10.3	254	10	US-09-925-302-596	Sequence 596, App

Sequence 4456, Ap Sequence 4, Appli Sequence 2083, Ap Sequence 3214, Ap	64002, 1813, 188300 137248	Sequence 3472 Sequence 312, Sequence 1247 Sequence 480,	Sequence 81, App. Sequence 82, Ap. Sequence 6, App. Sequence 166325 Sequence 62753,	quence 56/82, quence 187376, quence 16, App quence 1, Appl quence 58, App	equence 30, Applequence 1, Apply Quence 1, Appliequence 18, Appliequence 18, Applequence 888, Applequence 888, Applequence
US-10-106-698-445 US-10-076-069-4 US-10-276-774-208 US-10-104-047-321	-10-425-114-6 -10-369-493-1 -10-437-963-1 -10-437-963-1	0-224-99 0-421-13 0-374-78 0-755-88	S-10-042-02/-01 S-10-042-865-82 S-10-767-701-549 S-10-076-069-6 S-10-437-963-166	US-10-425-114-5678 US-10-437-963-1873 US-10-192-381-16 US-10-226-844-1 US-10-210-951-58 US-10-211-884-58	-10-211-030-3 -10-789-378-4 -10-741-600-1 09-871-889-1 -09-981-397A-
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and Polypeptides
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                                                                   APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PATENTIN Ver. 3.0

SEQ ID NO 5516

LENGTH: 157

TYPE: PRT
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Pred. No. 9.2e-64
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
US-10-106-698-5516
; Sequence 5516, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
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ilarity 98.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (55) CTHER INFORMATION: Xaa e; NAME/KEY: MISC FEATURE; LOCATION: (132); OTHER INFORMATION: Xaa e; US-10-106-698-5516
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE LOCATION: (55)
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Best Local Similarity
Matches 150; Conser
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SLGPRAPSLRRHVLIHNTLQQLQAALRLAPAPALPPEPLFLGEEDFSLSATIGSILRELD 103

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Signal Peptides
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                                                                                                                                         Gaps
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US-US-Y8-18-18-04A-568

Sequence 568, Application US/09978360A

Publication No. US20040110939A1

GENERAL IPCRRAWION:

APPLICANT: Edwards, Jean-Baptiste Dumas Milne

APPLICANT: Bougueleret, Lydie

APPLICANT: Clusel, Catherine

APPLICANT: Clusel, Catherine

APPLICANT: Clusel, Catherine

TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Sign

FILE REFERENCE: 56.U54 C.IP

CURRENT APPLICATION NUMBER: US/09/978,360A

CURRENT APPLICATION NUMBER: US 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

PRIOR PELICATION NUMBER: US 60/074,121

PRIOR FILING DATE: 1998-08-10

PRIOR PELICATION NUMBER: US 60/096,116

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-11-13

PRIOR FILING DATE: 1998-11-13

PRIOR FILING DATE: 1998-11-13

PRIOR PELICATION NUMBER: US 60/099,125

PRIOR PELICATION NUMBER: US 69/215,435

PRIOR APPLICATION NUMBER: US 09/215,435

PRIOR PELING DATE: 1998-11-17

PRIOR PELING DATE: 1998-11-17

PRIOR PELING DATE: 1998-11-17

PRIOR PELING DATE: 1998-12-17

PRIOR PELING DATE: 1998-12-17

PRIOR PELING DATE: 1999-12-17

PRIOR PELING DATE: 1
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                                                                                         Score 402; DB 14;
Pred. No. 1.1e-28;
); Mismatches 9
                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - ERWEWSPAGLOSYQOA
                                                                                                                                                                                                                                                                       TLQQLQAALRLAPAPALPPEPLFLGEEDF 89
                                                                                                                                                                                                                                                                                                                91
                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: MAP TO AC010271.5
; OTHER INFORMATION: EXPRESSED IN HELA,
US-10-029-386-33708
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nilarity 89.9%;
Conservative
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LOCATION: (28, 30, 40, 67,
OTHER INFORMATION: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SIGNAL LOCATION: -31...
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US-09-978-360A-568
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LENGTH: 236
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Best Local S
Matches 80
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Best Local S
Matches 76
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US-10-029-386-33709
i Sequence 33709, Application US/10029386
j Publication No. US20030194704A1
i GENERAL INFORMATION:
i APPLICANT: Penn, Sharron G.
i APPLICANT: Rank, David R.
i TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROF
i TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
i FILE REFERENCE: AEOMICA-X-2
i CURRENT PILING DATE: 2001-12-20
i CURRENT FILING DATE: 2001-12-20
i NUMBER OF SEQ ID NOS: 34288
i SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
i LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINGLE EXON NUCLEIC ACID TWO
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    GLDDFFLDIDTS
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Pred. No. 1.3e-50;
0; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 33708
LENGTH: 111
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US-10-029-386-33708
; Sequence 33708, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SII
; TITLE OF INVENTION: EXPRESSION ANALYSIS TW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AC010271.5; OTHER INFORMATION: EXPRESSED IN HELA, US-10-029-386-33709
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nilarity 96.8%;
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ORGANISM: DEATURE:
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US-10-296-115-1065

i Sequence 1065, Application US/10296115

i Sequence 1065, Application US/10296115

i Publication No. US20040053248A1

i GENERAL INFORMATION:

i APPLICANT: Hyseq Inc

i TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides

i FILE REFERENCE: 784PCT

i CURRENT APPLICATION NUMBER: US/10/296,115

i CURRENT FILING DATE: 2002-11-18

i PRIOR APPLICATION NUMBER: US09/488,725

i PRIOR FILING DATE: 2000-01-21

i PRIOR FILING DATE: 2000-04-25

i NUMBER OF SEQ ID NOS: 1478

i SEQ ID NO 1065

i LENGTH: 278
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LRHLVLVVNTLRRIQAS--MAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLED
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3.9e-11;
thes 69;
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4.8e-11;
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Mismatches
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                                                                                                                                                                                                                    213;
No. 3
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Pred. No.
                     60/187,470
                                                                                                                                                                                                                 Score
Pred.
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PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 412
LENGTH: 236
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32.6%;
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L-SHIEGLSQAPQP
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US-10-296-115-1065
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Sequence 412, Application US/09731872

Patent No. US20020102604A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Jobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SEC

FILE REFERENCE: 78.US3.REG

CURRENT APPLICATION NUMBER: US/09/731,872

CURRENT PILING DATE: 1999-12-08

PRIOR FILING DATE: 1999-12-08

PRIOR FILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 412

LENGTH: 236
                                                                                                                                  122 L-SHIEGLSQAPQP----LADEGPPGRSIGGXPPXLGALDLLGPATGCLLDNG
      GLKRKREEEEEKEPLAVDSW-WLDPGHAAVAQAPPAVASSSLFDLSVLKLHHSL
                                                                                                    -SSRYLGDSG
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APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY
FILE REFERENCE: 78.US4.CIP
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/731,872
                                                                                                                                                                                    176 DIDTSMYDNELWAPASEGLKPGPED---GPGKEEAPELDEAELDYLMDVLVGT
                                                                                                                                                                   DIDTSAVEKE --- PARAPPEP-PHNLFCAPGSWE----WNELDHIMEIILGS
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                                                                                                    LDTSMDGTEPPQNPVTPLGLQNEVPPQPD--
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Sequence 412, Application US/09876997
Publication No. US20030152921A1
GENERAL INFORMATION:
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76; Conser
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US-09-731-872-412
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               GLKRKHSDLEEEEERWEWSPA-GLOSYQQALLRISLDKVORSLGPRAPSLRRHVLIHNTL
                                                                              -LAP--APALPPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPO
                                                                                                    120 NSVSELPIVGSAPGORNPOSSLWEMDSPOENRGSFOKSLDOIFETLENK--NSSSVEELF
                                                                                                                                                                                                                 -APPEPPHNLFCAPGSWEWNELDHIMEII
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Pred. No. 0.0053;
1; Mismatches 88
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GENERAL INFORMATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Wandy, Christopher Robert
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: White, Jonathan
APPLICANT: Winle, Jonathan
APPLICANT: Rayner, William Nigel
APPLICANT: Rayner, William Nigel
APPLICANT: Rayner, William Nigel
APPLICANT: Ringsman, Susan Mary
APPLICANT: Kinge, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
CURRENT APPLICATION NUMBER: PCT/GB02/01662
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
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to. US20030203372A1
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nilarity 22.7%;
Conservative 34
                                                                                                                                               114 NPVTPLGLQNEVPPOPDP
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US-10-170-385-31
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LENGTH: 314
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ORGANISM:
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                                                                          Sequence 34001, Application US/10029386

; Sequence 34001, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PRO;

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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-GPGKEEAPELDEAELDYLMDVLVGT
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COTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.46
COTHER INFORMATION: SWISSPROT HIT: Q14140, EVALUE 2.70e-01
US-10-029-386-34001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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Pred. No. 0.00038;
2; Mismatches 86
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TITLE OF INVENTION: HEPP, A NOVEL GENE WITH A
FILE REFERENCE: 39532-176599
CURRENT APPLICATION NUMBER: US/10/076,069
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,923
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
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218 DIDTSMYDNELWAPASEGLKPGPED--
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Publication No. US20020177214A1
GENERAL INFORMATION:
APPLICANT: JURECIC, ROLAND
APPLICANT: NACHTMAN, RONALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 75; Conser
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                                                              US-10-029-386-34001
                                                                                                                                                                                                                                                                                               SEQ ID NO 34001
LENGTH: 222
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ORGANISM: Homo sapiens FEATURE:
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LENGTH: 254
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Best Local S
Matches 65
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Best Local S
Matches 65
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PGSWEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SSRYLGDS
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                       TLDDILFADIDTSMYDFDPCTSSSGTASKMAPVSADDLLKTLAPYSSQPVTPSQPFKMDL
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                                                                                                                                                        Sequence 627, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED
TITLE OF INVENTION: PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 0.0053;
34; Mismatches 88;
-ARAPPEPPHNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 596, Application US/09925302;
Patent No. US20020044941A1;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA104;
CURRENT APPLICATION NUMBER: US/09/925,302;
CURRENT FILING DATE: 2001-08-10;
PRIOR APPLICATION NUMBER: PCT/US00/05918;
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                 FILE REFERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
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GLDD-PFLDIDTSAVEKEP-
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Best Local Similarity 22.7%;
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin version
                                                                      302 TELDHIMEVLVGS
                                                       184 NELDHIMEIILGS
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US-10-755-889-627
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755-889<u>-</u>627
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US-09-925-302-596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 596, Application US/09925302
Publication No. US20030064072A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 0.21;
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                                                                                                                                                                                                                                 10.3%; Score 106; DB 5
25.6%; Pred. No. 0.21;
ive 32; Mismatches
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
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PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 896 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 596 LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KBY: SITE
; LOCATION: (105)
; OTHER INFORMATION: Xaa equals any
US-09-925-302-596
                                                                                                                                                                                  equals any
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larity 25.6%;
Conservative 3
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                                                                                                                                                                                                                                                                    Conservative
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US-09-925-302-596
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us-10-069-386a

GENE WITH A ROLE IN HEMATOPOIETIC AND NEURAL DEVELOR

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- NPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPCEGLEGLAPATPGPSSSCKS---DL
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                                                                                                                                                                                                                                                                                                                                      GLKRKHSDLEEEEERWEWSPAGLO---SY---OQALLRISLDKVQRSLGPRAPSLRRHVL
                                                                                                                                                                                                                                                                                                                                                      APGLGDGHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLDQIFETLETK-
Publication No. US20020177214A1
GENERAL INFORMATION:
APPLICANT: JURECIC, ROLAND
APPLICANT: NACHTMAN, RONALD
TITLE OF INVENTION: HEPP, A NOVEL GENE WITH
FILE REFERENCE: 39532-176599
CURRENT APPLICATION NUMBER: US/10/076,069
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,923
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
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Local Similarity 25.9%;
les 65; Conservative
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                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Job time : 135 secs
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Best Local S
Matches 65
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
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         -RLAP--APALPPEPLFLGEEDFSLSATIGSILRELDTSMDG
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                                                                                            124 AHPAPGLGDGHTOGPVSDLCPVTSAQAPRHLOSSAWEMDGPRENRGSFHKSLDO
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Pred. No. 0.21;
12; Mismatches 75;
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                                    IANTVRÓIÓEEMTQDGTWRTVAPQAAERAPXDRLVSTE
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                                                                                                                                                                                                                                                                                          Sequence 4456, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:
                                                                                                                            SRYLGDSGLDDFFLDIDTSAVEKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: MISC FEATURE
; LOCATION: (105)
; OTHER INFORMATION: Xaa equals any
US-10-106-698-4456
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US-10-076-069-4
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llarity 25.6%;
Conservative
                                                                 -PQNPVT-
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        IHNTLOQLQAAL
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 65; Conser
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US-10-106-698-4456
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LENGTH: 254
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141

-VFLEALSSRY

- PLGLQNEVPPQPDP

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111

57

Gaps

76;

Indels

79;

Score 105; DB 13; Pred. No. 0.25; L; Mismatches 79

31;

Length

228

- APPEPPHNLFCAPGSWEW

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5.1.6 Compugen Ltd
version - 2005
GenCore (c) 1993
        Copyright
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model 3 protein search, using • OM protein

•• 12:24:20 2005, 25, April on: Run

upda Search time 42 Seconds (without alignments) 348.362 Million cell up

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196

Title

....APGSWEWNELDHIMEIILGS US-10-069-386A-2 1033 1 MEGGLKRKHSDLEEEERWE... score: Sequence: Perfect

table Scoring

Gapext BLOSUM62 Gapop 10.0 ,

0.5

residue ведв, 74649064 513545 Searched:

513545 hits satisfying chosen parameters: of Total number

Minimum DB Maximum DB

2000000000 length: length: seq seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Patents Issued Database

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*/cgn2_6/ptodata/1/iaa/backfile81.pep:*/ •• •• 10 m 4 m 6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР				
Bult No.	Score	Ma	ength	\Box	ΙD	escription
-	5.	9.	N	4.	US-09-949-016-8918	«
7		•	ന	4	US-08-259-451-3	e 3, Appl
M		•	\mathbf{c}	٦	US-07-672-483-4	equence 4, Appl
4	93	0.6	2618	m	US-09-413-814-28	ence 28, Ap
ß		•	$\boldsymbol{\omega}$	വ	T-US95-04910-1	equence 13, App
y	σ	•		4	US-09-949-016-10257	10257,
7	0	•	~	4	85B-1	16, App
&	ö	•	4	7	-887-518-	2, Appl
6	ö	•	4	7	21-	equence 2, Appl
	。	•		~	7	2, Appl
	0	•	4	ო	-09 - 25	equence 1, Appl
12	90.5	•	947	4	US-09-871-889A-1	1, Appl
	0	•	~	4	-09-902-540-	equence 11750,
	φ.	•		4	-80-	equence 9, Appl
	9.	•		4	-09-949-016-7	equence 7139, A
	œ	•		4	-849-	equence 18, App
	88	•	\mathbf{c}	4	-976-59	280, Ap
		•	0	4	US-10-118-328-4	4, Appl
	9	•		4	-45	5, Appl
		•	4	゙゙゙゙゙゙゙゙゙゙゙	-910-	6798, A
		•	337	4	US-09-543-681A-7444	equence 7444, A
		•		゙゙゙゙゙゙゙゙゙゙゙	-09-25	equence 25281,
		•	2	4	US-09-345-473E-48	48, App
		•	-	4	49-016-11	11490,
		•		4	US-09-949-016-6276	ence 6276, A
		•	2152	സ	US-09-036-987A-3	Sequence 3, Appli
		•	2152	m	US-09-370-700-3	ence 3, Appl

3, Application US/08259451

RESULT 2 US-08-259-451-3

Sequence 3, Patent No.

Qι	Sequence 1, Appli	3, Ap	, App	Sequence 16, Appl	4, Ap	30, A	42, A	equence 18663,	Sequence 12, Appl	ppl	Q		Sequence 4, Appli	Sequence 4, Appli	Sequence 1, Appli	Ap	7646,
US-09-603-207-3	US-08-548-159-1	US-08-548-159-3	US-08-811-481-16	US-09-876-527-16	-09-538-09	US-09-949-016-9630	US-09-538-092-1142	-09-248-79	US-09-023-905A-12	US-08-466-390-4	US-08-470-950-4	US-08-467-781-4	US-08-195-487-4	US-08-483-924-4	US-09-452-294-1	PCT-US93-06160-4	US-09-949-016-7646
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                       Sequence 8918, Application US/09949016

Sequence 8918, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8918
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|----LGPAVRALGATFGPLL
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larity 23.4%;
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46; Conser
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,483
FILING DATE: 19910302
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/554,258
FILING DATE: 18-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HALEY Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: IAF8 C:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0674
                      Sequence 4, Application US/07672483
Patent No. 5359029
GENERAL INFORMATION:
APPLICANT: LACROIX, Martial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                   PEPTIDES
THEREOF F
VIRUSES
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: 875 Third Avenue
New York
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSE: FISH & NE
                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022-6250
COMPUTER READABLE FO
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                                                                                                                                                                                                                                                                                                                                                                                 Compositions for Detecting HTLV Infection
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ed. No. 0.71;
Mismatches
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Pred. No. (
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FILING DATE: 20-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,41
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
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                    Lee, Helen H.
Swanson, Priscilla A.
Idler, Kenneth B.
Rosenblatt, Joseph D.
Chen, Irvin S. Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Abbott Laboratories
One Abbott Park Road
                                                                                                                                                                                                                                                                                         Peterson, Bryan
Edwards, Michelle
Guidinger, Peggy
Tate, Cynthia
                                                                                                                                                                                                                                                                                                                                                                                                         and Assays
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                                                                                                                                                                                                                        Buytendorp, Mark H. Johnson, Joan E. Motley, Cheryl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Daniel W. Collins
REGISTRATION NUMBER: 31,912
REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
                                                                                                                            Golde, David W.
Robertson, Eugene
Stephens, John E.
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938-2623
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amino acid
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MEDIUM TYPE: Diskette,
MEDIUM TYPE: storage
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS
ADDRESSEE: Abbott L
                                                                                                                                                                                Stephens,
Chan, Emer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abbott Park
Illinois
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TITLE OF INVENTION:
TITLE OF INVENTION:
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INFORMATION:
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US-08-259-451-3
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                                         APPLICANT:
APPLICANT:
APPLICANT:
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Best Local S
Matches 40
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STATE:
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S AND ANALOGUES AND MIXTURES
FOR DETECTING ANTIBODIES TO HTLV-I
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Patent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Gesellschaft, Petra
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Best Local Similarity
Matches 40; Conser
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     CLASSIFICATION
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TOPOLOGY: unl
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APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER PILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 2618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 ALRLAP-APALPPEPLFLGEEDFSLSATIGSILRELDTSMDGTEPPQ---NPVTPLGLQN
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HIS VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION OF A NOVEL PRIMATE T-CELL LYMPHOTROPIC VIRUS AND THE USE OF THIS VIRU OR COMPONENTS THEREOF IN DIAGNOSTIC ASSAYS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                           2618;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                            Length
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States of America as represented
by the Secretary, Department of
Health and Human Services
VENTION: ISOLATION AND
                                                                                                                                                                                                                                                                                                                          Score 93; DB 3
Pred. No. 9.2;
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PLING DATE: 21-APR-1995
APPLICATION NUMBER:
FILTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1153 ADFFGIPPRDAEITDPQIRLLLECC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application PC/TUS9504910
GENERAL INFORMATION:
APPLICANT: The Government of the Un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                    ; ORGANISM: Sorangium cellulosum
US-09-413-814-28
                                                                                                                                                                                                                                                                                                                         9.0%;
illarity 25.5%;
Conservative 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 PARK AVENUE
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TITLE OF INVENTION: CHA
TITLE OF INVENTION: OR
TITLE OF INVENTION: OR
TITLE OF INVENTION: ANI
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                         QALLR---ISLD-
                                                                                                                                                                                                                                                                                                                                       l Similarity
55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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APPLICANT:
APPLICANT:
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Best Local
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Sequence 10257, Application US/09949016
Sequence 10257, Application US/09949016
Sequence 10257, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                 -- LPPEPLFLGEEDFSLSA
                                                                                                                                                                                                                                                                                                                                                                                                                     13 PKAP---RGLSTHHWLNFLQASYRLQPGPSDFDFQQLRRFLKLALKTPIWLNPIDYSLLA
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                            79;
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                                                                                                                                                                                                                                                                                                       Length 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EPANPPPL-
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Pred. No. 0.93;
23; Mismatches
                                                                                                                                                                                                                                                                                                                          0.99
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                                                                                                                                                                                                                                                                                                                               ed. No. 0.99
Mismatches
                                          26,728
R: 2026-4125PCT
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Pred. No. 0
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10257
LENGTH: 379
                                                                                                                                                                                                                                                                                                                         Pred
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                           19;
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ilarity 21.5%;
Conservative 1
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ilarity 21.6%;
Conservative 2.
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amino acids
                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amir
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Pred. No. 4.3;
7; Mismatches
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3200
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                      TECHNOLOGY LAW ST, SUITE 3200
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODFRATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5844073;
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins;
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                  SSEE: SCIENCE & TECHN
T: 268 BUSH STREET, 5
SAN FRANCISCO
: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 8.8%; Similarity 25.8%; 54; Conservative 1
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ADDRESSEE: SCIENCE & TECT
STREET: 268 BUSH STREET,
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: si
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                      ADDRESSEE:
STREET: 2
CITY: SAN
STATE: CA
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CITY: SA
STATE: C
COUNTRY:
ZIP: 941
                                                                                                         COUNTRY:
ZIP: 941
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Best Local S
Matches 54
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: WUKLEY, Paul
APPLICANT: TU, Jian
APPLICANT: XIAO, BO
APPLICANT: XIAO, BO
APPLICANT: LEAHY, Daniel
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN
FILE REFERENCE: JHU1580-4
CURRENT APPLICATION NUMBER: US/09/377,285B
CURRENT FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: TO COMMERCE TO COMME
  -EEETVASG
                                           TEPPONPVTPLGLONEVPPOPDPVFLEALSSRYLGDSGLDDFFLDIDTSAVEKEPARAPP
                                                                                      PDLQPP
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KPL-
                                                                                       -- DCSALDRD
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  -EGAAAAAASPTPSEDEEP--EEEEERAAAAEEG-
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                                                                                        -GPAGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
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                                                                                                                                                                             344 SGTSHFEFPDYCTPEVTEMIAGDW 367
                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09377285B Patent No. 6720175 GENERAL INFORMATION:
                                                                                                                                   -GSW
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Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Protei
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                                                                                       -SLGFLSRLPP
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NUMBER OF SEQ ID NOS: 72
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APPLICANT: Wu, Lin
TITLE OF INVENTION: 1
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US-08-887-518-2
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Matches 4
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3 GGLKRKHSDLEEEEERWEWSPAGLQSYQQALLRISLDKVQRSLGPRAPSLRRHVLIHNTL
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
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                                                         T97-008
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Patent No. 6265538
GENERAL INFORMATION:
INFORMATION:

V. RICHARD A

36,627
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                                                      REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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54; Conservative 1
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Similarity 25.8%;
54; Conservative 1
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                                            REGISTRATION NUMBER:
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; MOLECULE TYPE:
US-09-032-475-2
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SEQ ID NO 1
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Best Local S
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                  Version #1.30
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T: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
: CALIFORNIA
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/032,475

FILING DATE:
                                                                                                 US/08/887,518
                                            US/09/023,321
                                                                                                                                                                  -008
                   Release #1.0,
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; Sequence 2, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins,
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY
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                                                                                                                                     NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97
TELECOMMUNICATION INFORMATION:
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415) 343-4342
SEQ ID NO: 2:
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ilarity 25.8%;
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                 SOFTWARE: Patentin Re
CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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PRIOR APPLICATION DATA:
                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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; MOLECULE TYPE:
US-09-023-321-2
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                                                         FILING DATE:
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INFORMATION FOR
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE INFAMMATORY RESPONSE INDUCED
                                                                                                                                   QQLQAALRLAPAPALPPE----PLFLGEEDFSLSATIGSILRELDTSMDGTEPPQNPVT
                                                                                                                                                                                                     --LGDSGLDDFFLDIDTSAVEKEPA
                                                                                                                                                                                                                      P-ERKATVPEQELQQLEIELFLNSLSQPFSLEEQEQILSCLSIDSLSLSDDS---EKNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TLHAOPRELSPRAPGPRPAEETTGRA
                                                                 GGLKRKHSDLEEFEERWEWSPAGLQSYQQALLRISLDKVQRSLGPRAPSLRRHVLIHNTL
                                                                                      --PLFLGEEDFSLSATIGSILRELDTSMDGTEPPQNPVT
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 Length
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DB 2;
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Score 90.5; DB Pred. No. 4.3; 7; Mismatches
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Pred. No. 4.3;
7; Mismatches
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APPLICANT: Lin, Xin
APPLICANT: Lin, Xin
APPLICANT: Gelezuinas, Romas
TITLE OF INVENTION: A NOVEL INHIBITOR OF THE
TITLE OF INVENTION: BY TNF-ALPHA AND IL-1
FILE REFERENCE: 30448.61USU1
CURRENT APPLICATION NUMBER: US/09/257,703
CURRENT FILING DATE: 1999-02-25
EARLIER FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
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                                                                                      Gaps
                                                                                     57;
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                                                      Length
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FUSED DNA SEO
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ORGANISM: RECOMBINAL.
PUBLICATION INFORMATION:
AUTHORS: NOBUYUKI FUJII ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
TITLE: EXPRESSING SAID FUSED PROTEIN
                                                                                                                                                                                            GSILRELDTSMDGTEPPQNPVTPLGLQNEVPPQPDPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                      55;
                                                     4 ;
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                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JEFFERSON DAVIS HIGHWAY,
                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08778717
; Patent No. 6602689
; GENERAL INFORMATION:
; APPLICANT: UENO, EIICHI
APPLICANT: NOBUYUKI, FUJII
APPLICANT: OKADA, MASAHISA
; TITLE OF INVENTION: EXPRESSED FROM SAID FU
; TITLE OF INVENTION: EXPRESSING SAID DNA SE
; TITLE OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 352225/1995
FILING DATE: 28-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2084-031-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                   Score 90.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,71
FILING DATE: 12-DEC-1996
                                                                                   12;
                                                     8.8%;
; ORGANISM: Myxococcus xanthus US-09-902-540-11750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                           271 LDLSDAEAAPPPRAP-
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SEQUENCE CHARACTERISTICS
                                                                                      Conservative
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ADDRESSEE: P.C.
STREET: 1755 S. JEF
CITY: ARLINGTON
STATE: VA
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Best Local Similarity
Matches 42; Conser
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ORIGINAL SOURCE:
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Fatent No. 6645726

GENERAL INFORMATION:

APPLICANT: Greene, Warner C.

APPLICANT: Lin, Xin

APPLICANT: Lin, Xin

TITLE OF INVENTION: IL-1

FILE REFERENCE: 30448.61USDI

CURRENT APPLICATION NUMBER: US/09/871,889A

CURRENT APPLICATION NUMBER: 09/257,703

PRIOR FILING DATE: 1999-02-25

PRIOR FILING DATE: 1998-02-27

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.1
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US-09-902-540-11750

i Sequence 11750, Application US/09902540

j Patent No. 6833447

j GENERAL INFORMATION:

j APPLICANT: Goldman, Barry S.

j APPLICANT: Hinkle, Gregory J.

j APPLICANT: Wiegand, Roger C.

j TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses

j FILE REFERENCE: 38-10(15849)B

j CURRENT APPLICATION NUMBER: US/09/902,540

j CURRENT FILING DATE: 2001-07-10

j PRIOR FILING DATE: 2000-07-10

j WIMDER OF CO.
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SEQ ID NO 11750
LENGTH: 1027
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54; Conser
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US-09-949-016-7139
US-09-949-016

Sequence 7139, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 7139
LENGTH: 611
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                                                                                                                                                                       -LPPEPLFLGE
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                                                                                                                                                                                                                                                  61;
                                                                                                            EGGLKRKHSDLEEEE----ERWEWSPAGLQSYQQALLRISLDKVQRSLG--
                                               Length 215;
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 9: FROM 1
                                             Score 89.5; DB Pred. No. 0.78; 24; Mismatches
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                                                                                                                                                                      -PRAPSLRRHVLIHNTLOOLOAALRLAPAPA-
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 RESIDUES IN SEQ ID NO:
                                             Query Match
Best Local Similarity 23.7%;
Matches 41; Conservative 2
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US-08-778-717-9
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	80
	69	00	591	9	AX088925	AX088925 Sequence
.,		100.0	1542	თ	AF192529	AF192529 Homo sapi
m	589	99.7	1325	9	CQ783944	CQ783944 Sequence
4	589	99.7	32	φ	BD127913	BD127913 Primer fo
u1	58	99.7	1325	თ	AK074604	AK074604 Homo sapi
Ψ	589	99.7	1346	თ	BC014061	
17	589	99.7	1420	თ	BC050643	
w	589	99.7	1536	9	CQ731553	71
U	589.	99.7	160643	თ	AC010271	AC010271 Homo sapi
	588.	Φ	825	9	CQ779981	CQ779981 Sequence
11	588	99.6	825	9	CQ781937	CQ781937 Sequence
	588.	99.6	825	9	BD124690	90
	588.	99.6	825	9	BD126646	BD126646 Primer fo
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	47	0	206	9	CQ463286	CQ463286 Sequence
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	429.	72.6	257945	7	AC112313	AC112313 Rattus no
	429.	72.6	290929	7	AC118914	AC118914 Rattus no
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	4	2	•	6942	7	AC100015	15 Mt
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RESULT 1 AX088925 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL FEATURES SOURCE	AX088925 Sequence 1 from Patent W00114546. AX088925 AX088925 AX088925.1 GI:13397684 unidentified unidentified unidentified unclassified. 1 Alaoui-Jamali,M.A. and Cho,J.M. Replication protein a binding transcriptional uses thereof Patent: WO 0114546-A 1 01-MAR-2001; Centre for Translational Research in Cancer (C Location/Qualifiers 1. 591 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" /note="replication protein A transcri	DNA linear Phascriptional in A transcriptional	<pre>factor (rbt1) and .A) ptional factor"</pre>
Query Match Best Local Matches 59	ch 100.0%; Score 591; DB 6; il Similarity 100.0%; Pred. No. 7.3e-120; 591; Conservative 0; Mismatches 0;	Length Indela	591; , 0; Gaps 0;
Qy Dp	1 ATGGAGGGAGGCTTGAAGAGGAAACACTCTGATTTGGAAGAGGAGGAGGAGGAGGGGGGGG	atttggaagaggaggag 	SAGAGGTGGGAG 60 SAGAGGTGGGAG 60
\$ 9. \$0.	61 TGGAGTCCAGCAGGCCTTCAGAGCTACCAGCAAGCCCTGCTCCGCATCTCCCTAGACAAA	AAGCCCTGCTCCGCATC: 	
Oy 121 Db 121	11 GTCCAGCGCAGCCTGGGCCCCCGAGCACCCCGCAGGCATGTCCTCATACCATAAC	sccrcccaagcargrc(CTCATCCATAAC 180
Qy 181	11 ACCCTCCAACAGCTGCAGGTGCACTTCGCCTGGCTCCCGCCCTGCCCTGCCCCCGAG 240	rescrecesecerece	CTGCCCCCGAG 240

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DTSMDGTEPPQNPVTPLGLQNEVPPQPDPVFLEALSSRYLGDSGLDDFFLDIDTSAVE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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        ATGGAGGGAGGCTTGAAGAGGAAACACTCTGATTTGGAAGAGAGGAGGAGGAGGTGGGAG
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                        Koga, H.
Primers for synthesizing full length cDNA clones and their Patent: EP 1396543-A 4084 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1542)
Cho, J.M., Song, D.J., Bergeron, J., Benlimame, N., Wold, M.S. &
Alaoui-Jamali, M.A.
RBT1, a novel transcriptional co-activator, binds the secon
subunit of replication protein A
Nucleic Acids Res. 28 (18), 3478-3485 (2000)
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QC H3T-1E2,
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ACCCTCCAACAGCTGCAGGCTGCACTTCGCCTGGCTCCCGCCCCTGCCCTGCCCT
                                                                            GAGCTGGACACCTCCATGGATGGGACTGAGCCCCCTCAGAATCCAGTGACTCCC
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Cho,J.M., Song,D.J. and Alaoui-Jamali,M.A.
Direct Submission
Submitted (06-OCT-1999) Experimental Medicine,
Institute, 3999 Cote-Ste-Catherine, Montreal,
Location/Qualifiers
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Pred. No. 6.4e-120;
; Mismatches 0;
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Homo sapiens RPA-binding trans-activator AF192529
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'mol_type="mRNA"
'db_xref="taxon:9606"
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AK074604

Homo sapiens cDNA FLJ90123 fis, clone HEMBA1007226, highly similar to Homo sapiens RPA-binding trans-activator (RBT1) mRNA.

AK074604

AK074604.1 GI:22760150

oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
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                                                             C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/ner for synthesizing full-length cDNA and use thereof FH Location/Qualifiers
CDS (93). (680).
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Pred. No. 1.5e-119;
0; Mismatches 1;
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/organism="Homo sapiens
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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CHI KOJIMA,
TETSUJI OTSUKI, HISASHI
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Best Local Similarity 99.8%;
Matches 590; Conservative
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Primer for synthesizing full-length cDNA and use thereof.

BD127913.1 GI:23222858

JP 2002017375-A/3344.

Homo sapiens (human)

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ca, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3344 22-JAN-2002;
HELIX RESEARCH INSTITUTE
                                                                                         ATGGAGGGAGGCTTGAAGAGGAAACACTCTGATTTGGAAGAGGAGGAGGAGGAGGAGGAGGG
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ISHII,
YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEII
                                        Length
                                                                Indels
 KEPARAPPEPPHNLFCAPGSWEWNELDHIMEIILGS
                                     Query Match
Best Local Similarity 99.8%; Pred. No. 1.5e-119; Matches 590; Conservative 0; Mismatches 1;
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JP 2002017375-A/3344
22-JAN-2002
07-JUL-2000 JP 200025
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PRI 03-SEP-2002 highly similar mRNA.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 28 Row: f Column: 10
This clone was selected for full length sequencing because it
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                                                                                                                                                                            Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).

Location/Qualifiers
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Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1007226"
/tissue_type="whole embryo, mainly head"
/clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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/note="cloning vector: pME18SFL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 589.4; DB 9;
Pred. No. 1.5e-119;
0; Mismatches 1;
                                                                                                         NEDO human cDNA sequencing project
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Isogai, T. and Otsuki, T.
Direct Submission
Submitted (25-MAR-2002)
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Matches 590; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

I (bases 1 to 1346)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klaudiner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerztion and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

L. Proc., Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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UINH-MGC Project URL: http://mgc.nci.nih.gov

On Aug 19, 2003 this sequence version replaced gi:15559388.

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                          PRI 29-JUN-2004 variant 2, mRNA
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Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                           683
                                            TGGGAGTGGAATGAACTGGATCACATCATGGAAATCATTCTGGGGTCCTAA
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens SERTA domain containing 3, transcript (cDNA clone MGC:19994 IMAGE:3926937), complete cds. BC014061.
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matched
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product="RPA-binding trans-activator"
protein_id="AAH14061.1"
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                                                                                                                                                                                                                                                        xref="LocusID:29946"
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db_xref="LocusID:29946
ection
                                                                                                                    note="Vector: pOTB7
following select ocation/Qualifier
                                                                                                                               . .1346
gene="SERTAD3"
                                                                                                                                                                                              gene="SERTAD3"
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Best Local Similarity 99.8%;
Matches 590; Conservative
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
Homo sapiens SERTA domain containing 3, transcript variant 2, mRNA (cDNA clone MGC:60134 IMAGE:6503515), complete cds.
BC050643.2 GI:3419111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 110 Row: o Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718683.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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On Aug 25, 2003 this sequence version replaced gi:29791864.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R. Direct Submission

Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Mammalia; Eutheria;
1 (bases 1 to 1420)
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Catarrhini; Hominidae; Homo
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Pred. No. 1.4e-119
; Mismatches 1
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chromosome 19 clone
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Homo sapiens
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Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 160643)
DOE Joint Genome Institute and S
Direct Submission
Unpublished
2 (bases
                             cent: WO 02068579-A 17487
Corporation (NY) (US)
Location/Qualifiers
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transcripts,
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AC010271.8 G:HTG.
Kits, such humanexons thereof Patent: WO PE Corporat.
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KEPARAPPEPPHNLFCAPGSWEWNELDHIMEIILGS"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W
                                                                                                                                                   Score 589.4; DB 9;
Pred. No. 1.5e-119;
0; Mismatches 1;
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17487 from Patent WO02068579
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.68_..758
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ilarity 99.8%;
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Sequence 17
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                                                                                                                                                                Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Primers for synthesizing full length cDNA clones and their Patent: BP 1396543-A 121 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
1. 825
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 2.6e-119;
0; Mismatches 2;
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121 from Patent EP1396543
                                                                                                                                                   GI:45536053
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Best Local Similarity 99.7%;
Matches 589; Conservative
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Submitted (13-JUL-2002) DOE Joint Genome Institute, 2800
Drive, Walnut Creek, CA 94598, USA
On Jul 13, 2002 this sequence version replaced gi:158872'
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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                 Facility,
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Direct Submission
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                                                                                     Genome Institute,
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DOE Joint Genome Institute and Stanford Human Genom
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         Direct Submission
Submitted (15-SEP-1999) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
3 (bases 1 to 160643)
DOE Joint Genome Institute and Stanford Human
                                                                                                                                                                                                                                                                                       www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.1.
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Pred. No. 7.9e-120
0; Mismatches 1
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Submitted (29-AUG-2000) DOE Joint
Drive, Walnut Creek, CA 94598, US
4 (bases 1 to 160643)
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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Genome Institute
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ilarity 99.8%;
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Pred. No. 2.6e-119;
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2077 from Patent EP1396543
                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                          GI:45537993
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                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Homo.

1 (bases 1 to 825)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 121 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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JP 2002017375-A/121
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI
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Pred. No. 2.6e-119;
0; Mismatches 2;
825 bp DNA
full-length cDNA
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JP 2002017375-A/121.
Homo sapiens (human)
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                                                                                                                                                                                          consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                           Center clone name: 384 E o

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 145359 bases at least Q40

Consensus quality: 155420 bases at least Q30

Consensus quality: 159351 bases at least Q20

Insert size: 161352; sum-of-contigs

Quality coverage: 4.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                       sum-of-contig
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5880
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clone_lib="RPCI-11 Human Male BAC"
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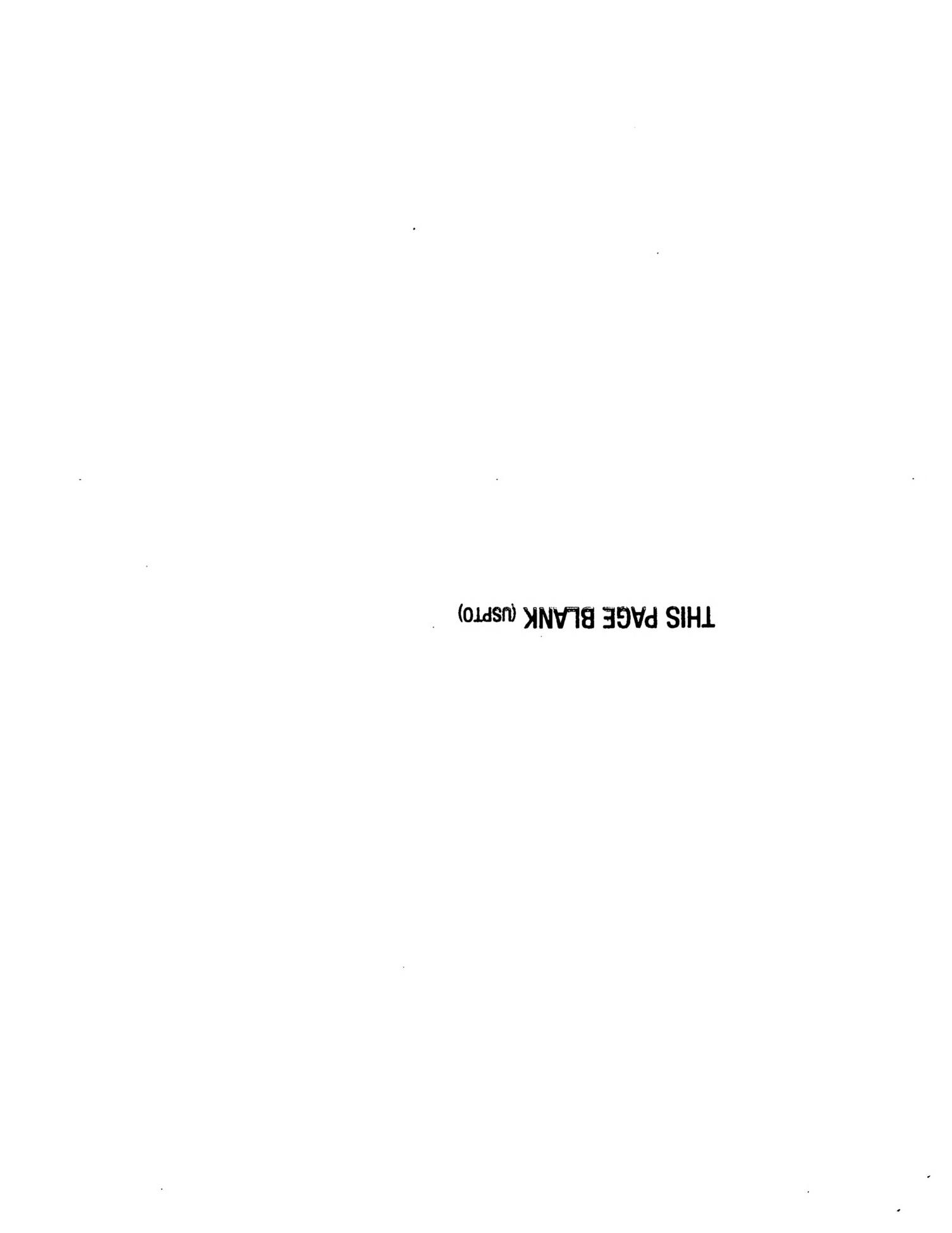
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                                                                                                              Score 584.6; DB :
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                                                                                                Score 473; DB 6;
Pred. No. 7.4e-94
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  06-DEC-2001
                                  1. .506
/organism="Homo sapiens"
/mol_type="unassigned DNA
/db_xref="taxon:9606"
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Location/Qualifiers
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Compugen Ltd
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- 2005
GenCore (c) 1993
        Copyright
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- nucleic search, using sw model OM nucleic

•• 03:13:57 2005, 26, April on

Run

Search time 425 Seconds (without alignments) 8231.923 Million cell updates/sec

US-10-069-386A-1 591 score: Title: Perfect

...aaatcattctggggtcctaa 1 atggagggaggcttgaagag... Sequence:

591

1.0 Gapext IDENTITY NUC table: Scoring

residues 2959870667 4390206 seqs, Searched:

8780412 hits satisfying chosen parameters: of Total number

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Database

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SUMMARIES

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Result No.	Score	Query Match	Length DB	DB	ΩI	Description
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4	. 68	φ.	1515	13	ADQ85787	37
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	76.	7	σ	4	AAH34147	Aah34147 Human col
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ALIGNMENTS

RBT1; replication protein A binding transcriptional activator 1; RPA32; gene therapy; apoptosis; cancer; leukaemia; ds. Replication protein A binding transcriptional activator 1 RBT1 gene. Location/Qualifiers
1. .591
/*tag= a
/product= "RBT1" ВР 591 (first entry) AAF28052 standard; DNA; WO200114546-A2 Unidentified 23-MAY-2001 01-MAR-2001. AAF28052; Key RESULT 1 AAF28052 CCXEXETTTTXSXEXEXEXEXEXEXEXEXEXEXEXEX

2000WO-CA000948 17-AUG-2000;

(TRAN-) CENT TRANSLATIONAL RES IN CANCER 99US-0149472P. 19-AUG-1999;

Cho JM; Alaoui-Jamali MA,

WPI; 2001-218447/22. P-PSDB; AAB35402.

1 gene, gene Novel replication protein A binding transcriptional activator 1 useful for treating neoplastic disorders such as cancer and in 9 therapy.

Claim 1; Fig 1; 16pp; English.

The present invention provides the protein and coding sequences of the replication protein A binding transcriptional activator 1 (RBT1). The

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protein is capable of inducing apoptosis. The sequences are usefigene therapy and other methods of treatment of cancer, including leukaemias. The present sequence is the RBII coding sequence
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The invention relates to primers for synthesising full length cDNA clones. 830 .cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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2000JP-001
                                        Nishikawa T, ]
w A, Sugiyama
                                                                       WPI; 2001-524255/58
P-PSDB; AAM93922.
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Nagai K, Kojima
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2000JP-00183865.
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02-MAY-2000;
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a chimeric polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; tumour-associated antigenic target; TAT; cytostatic; gene therapy cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3 a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
AAGGAGCCTGCACGGGCCCCAGAGCCTCCTCACAACCTCTTCTGTGCCCCAGGTTCT
                                                                                               CDNA sequence #2601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule and encoded polypeptide, for diagnosing,
preventing or treating cell proliferative disorders such as cancer
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comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein; where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the protein a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above corganic molecule to a cell that expresses the protein described above.

The TAT sequences have cytostatic activities, and can be used in gene of the containing the protein; and (17) a method of cativities, and can be used in gene organic molecule to a cell that expresses the protein described above.
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This invention relates to novel methods for diagnosing and monitoring autoimmune and chronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic tools for the management of, in particular, patients with systemic lupus erythematosis (SLE) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in a concerted manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the disease in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma, ankylosing spondylitis, ulcerative colitis, primary sclerosing cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis. This polynucleotide is a DNA sequence representing human mRNA that is differentially expressed in patients with SLE, used in an exemplification
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                                                                                                                                               systemic lupus erythematosis; rheumatory disease; SLE; Sjogren's lupus erythematosis; rheumatoid arthritis; cholecystitis; Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis; ulcerative colitis; primary sclerosing cholangitis; appendicitis; diverticulitis; primary sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one more genes.
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libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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Best Local Similarity 99.7%;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers chable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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                                                                          Hayashi K,
K, Kojima
                                                                                                                                                                                                                                                                                                                                                C; 230 G; 183
                                                                                                                                   full
                                                                                                                                  830 Primers useful for synthesizing
                                                                           ai T,
Nagai
                                                                                                                                                                                                                                                                                                                                                                                          0;
          99JP-00194486
2000JP-00118774
2000JP-00183765
                                                                           awa T, Isogai
Sugiyama T, N
                                                                                                                                                                                                                                                                                                                                                                   Match 99.6%;
Local Similarity 99.7%;
nes 589; Conservative
                                                                                                                                                                                                                                                                                                                                                825 BP; 160 A; 247
                                                                                                                                            manipulation.
                                                      RES INST
                                                                                                                                                                    Example 11; SEQ ID NO
                                                                                                             2001-524255/58
                                                                           Nishikawa
                                                      (HELI-) HELIX
          08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                       Wakamatsu A,
                                                                                                                                               in genetic
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                                                                                                                                                                                                                                                                                                                                                Sequence
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is the 3' end of a representative human DNA cluster of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCTCCAACAGCTGCAGGCTGCATTCGCCTGGCTCCCGCCCTGCCCTGCCCCCGAG
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                                                                                                                                                       transcription;
                                                                                                                                                                                                                                                                                                                                            Kawai Y;
T, Koga
                                                                                                                                                                                                                                                                                                                                                                                               synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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         TGGGAGTGGAATGGATCACATCATGGAAATCATTCTGGGGTCCTAA
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3, Otsuki
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                                                                                                                                                        glycoprotein;
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Pred. No. 2e-134;
0; Mismatches 2;
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Kojima
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K, Koji
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                                                                                                                                    representative human cDNA
                                                                                                                                                       transduction;
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a T, Nagai
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2000JP-00118774.
2000JP-00183865.
2000EP-00114089.
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Best Local Similarity 99.7%;
Matches 589; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              New oligonucleotide primers
length human cDNAs.
                                                                      82
                                                                                                                                                                 method; ss.
                                                                       CDNA;
                                                                                                                                                       signal
                                                                                                                                                                                                                                                                                                                                                       Sugiyama
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11-JAN-2000;
02-MAY-2000;
07-JUL-2000;
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T, Koga
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                CCCCTCTTCCTGGGCGAGGATTTCTCCCTGTCAGCCACCATTGGCTCTATC
                      CCCTCTTCCTGGGCGAGGATTTCTCCCTGTCAGCCACCATTGGCTCTATC
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S, Otsuki
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K, Kojima
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                                                                                                                                                                                                                                                                                    SegID
                                                                                                                                                                                                                                                                                                   signal transduction;
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a T, Nagai
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2-MAY-2000;
7-JUL-2000;
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                 82
                Length
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ů;
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The invention relates to a nucleic acid probe for measuring human gene sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences (ully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expression thuman cells or tissues. Also included are a spatially-cadressed in human cells or insulative of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon microarray for measuring human gene expression, a vector comprising the single exon microarray for measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid sequences (petionally with conservative amino acid substitutions), and sequences (petionally with conservative amino acid substitutions), and a customer desiring to measure gene expression, a method of providing a customer desiring to measure gene expression and apparatus are useful in gene expression and apparatus are useful in gene expression analysis. The probe may subscription, and a computer-readable cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expression of a single exon microarrays.

In addition, the probes are used in identifying and characterising gross alterations in the probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their contain the probes are used in identifying and characterising general electrons in the genomic locus that includes their exon, in assessing smaller genomic alterations, in detecting and the survey or i
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                                                                                                                              derived single exon nucleic acid probes useful nalysis, for identifying or characterizing alter assessing genomic alterations or as tools
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Pred. No. 5.3e-132;
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                                                                                                                                                                                                                       Claim 1; SEQ ID NO 24898; 80pp; English.
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자
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal 539 306 419 c acids encoding 4277 human colon cancer-associated polypeptides, for preventing, diagnosing and/or treating colorectal cancers. GGAGCTGGACACCTCCATGGATGGGACTGAGCCCCCTCAGAATCCAGTGACTCCCCTTGG GTACTTGGGGGACTCTGGCTGGATGACTTCTTTCTGGACATTGACACATCTGCGGTAGA CCTCCAGAATGAAGTGCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCCG AAAGGAGCCTGCACGGGCCCCACCAGAGCCTCCTCACAACCTCTTCTGTGCCCCAGGTTC AAAGGAGCCTGCACGGGCCCCAGCAGCCTCCTCACAACCTCTTCTGTGCCCCCAGGTTC 591 cancer antigen; diagnosis; detection; TTGGGAGTGGAATGAACTGGATCACATCATGGAAATCATTCTGGGGTCCTAA encoding cDNA SEQ ID NO:1229 Rosen CA; Claim 1; Page 3003-3004; 9803pp; English BP Birse CE, AAH34147 standard; cDNA; 1596 99US-0157137P 99US-0163280P 2000WO-US026524 SCI INC cancer; colon antigen (first entry) Human; colon cancer; colo colorectal carcinoma; ss. Ruben SM, Barash SC, (HUMA-) HUMAN GENOME WPI; 2001-235357/24. P-PSDB; AAG74742. cancer WO200122920-A2 Homo sapiens 28-SEP-2000; 29-SEP-1999; 03-NOV-1999; colon 03-SEP-2001 05-APR-2001 540 307 480 487 300 360 367 420 427 547 Nucleic useful f RESULT 1: S S qq ò Š 셤 ò Š

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carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
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                                                           Score 576.2; DB 4;
Pred. No. 2.3e-131;
2; Mismatches 0;
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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (II) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample from a patient with (IV), detecting the amount of polynucleotide sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCCAGAATGAAGTGCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 506;
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Pred. No. 3.6e-106;
0; Mismatches 5;
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Local Similarity 98.6%;
les 488; Conservative C
2000US-0207484P
                                                                SL,
                                                              Harlocker
                                                                                              WPI; 2002-122075/16.
                              (CORI-) CORIXA CORP
                                                                                                                                                                                                             Claim 1; SEQ ID NO
26-MAY-2000;
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Matches 488
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The present invention describes a composition (I) comprising: carriers and immunostimulants, and a polypeptide (II) of a ovarian tumour colypeptide encoded by a polymucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polymucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
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                                                                                                                                                                                                                                          Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                           clone SEQ ID NO:6239
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                                                                                                                                                                                                           cancer related cDNA
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon probes cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acids of any of the above- mentioned amino acids of selling and/or licensing single exon probes or microarrays to sequences (optionally with conservative amino acid substitutions), and isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe
                      118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
CCAGCGC - CCTGGGCCCCCGAGCACCCAGCATCCATGTCCTCATACAC
                                                                        CCTCCAACAGCTGCAGGCTGCACTTCGCCTGGCTCCCGCCCTGCCCTGCCCCCGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                     exon probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                  s; ss; gene expression; single exon
splicing event; genomic alteration
                                                                                                                                                                                                                                                                                                                                                                 derived single exon probe #11178.
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(RANK/) RANK D R.
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expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                     seqdata.uspto.gov/sequence.html?DocID=20030194704
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The invention relates to an isolated nucleic acid comprising at least 85% identity to either of 2 2082 base pair sequences, given in the specification. The nucleic acids and polypeptides of the invention are useful for detecting, treating and preventing neurodegenerative diseases such as amyotrophic sclerosis, and haematological disorders, particularly neoplasms of the blood such as acute myelomnocytic leukaemia, particularly in plasms of the blood such as acute myelomnocytic leukaemia, clymphoblastic leukaemia, adult T-cell lymphoma/leukaemia, diffuse large Brotlicular lymphoma, nodal marginal zone B-cell lymphoma, Burkitt's lymphoma, splenic marginal zone B-cell lymphoma, mantle cell lymphoma, splenic marginal zone B-cell lymphoma, mantle cell lymphoma, splenic cell types present in the biological sample. The mammal is useful in screening drugs for treating the disorders cited above, and for testing of novel haematopoietic cytokines/growth factors for mobilisation and differentiation of stem and progenitor cells. The nucleic acids of the invention can be used in gene therapy. This polynucleotide sequence represents the mouse haematopoietic progenitor protein (Hepp) gene of the
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                                                                                            useful
                                                                                           New hematopoietic progenitor protein (Hepp) genes and proteins, useful for detecting, treating and preventing neurodegenerative diseases, e.gamyotrophic sclerosis, and hematological disorders, e.g. neoplasms of
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Search time 155 Seconds (without alignments) 6238.965 Million cell updates/sec •• 06:54:54 2005, 26, April Run on:

US-10-069-386A-1 591 1 atggagggaggcttgaagag score: Title: Perfect

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Issued Databas

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SUMMARIES

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ALIGNMENTS

RESULT 1

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Version #1.25
             Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                          Suite 500
                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30472/114
                                                                                                                                                NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, S
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TUBE: nucleic acid
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US-08-232
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US-09-733-294A-30/c
; Sequence 30, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
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ilarity 50.4%;
Conservative
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Best Local Similarity
Matches 139; Conser
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FEATURE:
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136;
Similarity 5.8%; Pred. No. 0.0018; 24; Conservative 215; Mismatches 173;
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FastSEQ for Windows

; NAME/KEY: misc_feature
; LOCATION: (1)...(44952)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-12197

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LENGTH: 44952
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US-09-949-016-17583/c

Sequence 17583, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES;

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
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Patent No. 6794363
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
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Pred. No. 0.066;
0; Mismatches 74;
         CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
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US-09-249-585A-2/c
; Sequence 2, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTER
; FILE REFERENCE: 0867/0D905
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| Similarity 54.0%;
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ENGTH: 1603
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ore 41; DB 3 ed. No. 0.2; Mismatches
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APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399; CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
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   Score 41;
Pred. No. (
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APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Pro; TITLE OF INVENTION: System
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ORGANISM: Epstein-Barr
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SEQ ID NO 3
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r, Suite 3400
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Pred. No. 0.22;
0; Mismatches
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ADDRESSEE: Flehr, Hobbach, Tee
STREET: 4 Embarcadero Center,
                                                                                                                                                                                                                                                       ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
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30-MAR-1998
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ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NDENCE ADDRESS:
SEE: Flehr, Hohbach, Tee
: 4 Embarcadero Center,
San Francisco
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TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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Patent No. 6316223
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Silva, Robin M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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; MOLECULE TYPE:
US-09-050-863-2
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US-09-359-081-2/c
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; Sequence 1, Application US/09130114
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaj, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Ger;
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/1D903US1
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/050,863

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 949-8711

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
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                                                                                      APPLICATION NUMBER: US/09/359,08:
FILING DATE: 22-Jul-1999
CLASSIFICATION: <Unknown>
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TOPOLOGY: unknown
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MOLECULE TYPE: DNA
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SEQUENCE DESCRIPTION: SEQ ID NO:
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US-09-64/--.

US-09-64/--.

Sequence 14, Appl.

Sequence 14, Appl.

Patent No. 6586180

GENERAL INFORMATION:

APPLICANT: Ruffner, Duane E.

APPLICANT: Chen, Zhidong

TITLE OF INVENTION: Directed Antisense Libraries

TITLE OF INVENTION: Directed Antisense Libraries

FILE REFERENCE: T6678.PCT.US

CURRENT APPLICATION NUMBER: DC7/US99/06742

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 1999-03-28

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 14

TENGTH: 8705
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Patent No. 6251433
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
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Pred. No. 0.37;
0; Mismatches
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Similarity 51.4%;
95; Conservative
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US-09-647-344A-14
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Best Local S
Matches 95
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TITLE OF INVENTION: Compositions and Methods for
Polynucleotide Delivery
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                                                                                                                                                                                                                                                                                 #1.30
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STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
IPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
RENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,925
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                                                                                                                                                                                                                                                                                   Version
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Pred. No.
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                                                                                                                                        LDM PC COMPATIBLE

OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vacuremy APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
FILING DATE:
CLASSIFICATION: 514
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NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Patent No. 6468986
GENERAL INFORMATION:
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CITY: Emeryville
STATE: California
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                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS
ADDRESSEE: Chiron
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nucleic acid
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Best Local Similarity
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                               COUNTRY: U.S.A. ZIP: 94608-2916
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 REFERENCE/DOCKET TELECOMMUNICATION :
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Best Local Similarity
Matches 95; Conser
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US-07-884-811-15
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ANTS
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Patent No. 5316921
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie
TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                           CCAGCAGGCCTTCAGAGCTACCAGCAAGCCCTGCTCCGCATCTCCCTAGACAAA
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                                                                                                                                                                                                                                                                                                                  Score 41; DB 3;
Pred. No. 0.39;
0; Mismatches
                                      APPLICATION NUMBER: 08/910,647
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 5.25 inch, 360 Kb floppy OPERATING SYSTEM: PC-DOS/Ms-DOS
                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 1
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19920518
                <Unknown>
                                                                                                                                                                                               LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 21-Jul
CLASSIFICATION: <Un
PRIOR APPLICATION DATA:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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larity 51.4%;
Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,
                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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US-07-884-811-15/c
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Californ:
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Pred. No.
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MEDIUM TYPE: 5.25 inch, 360 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/07885971
Patent No. 5328837
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19920518
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                               NUCLEIC ACID
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APPLICATION NUMBER:
FILING DATE:
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                                               Query Match
Best Local Similarity 51.4%; Pred. No. 0.4;
Matches 95; Conservative 0; Mismatches 90; Indels
; STRANDEDNESS: single
; TOPOLOGY: linear
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Search completed: April 26, 2005, 10:14:01 Job time : 161 secs

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2: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{VSOT} \)\text{NEW PUB.seq:*} \\
3: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{VSO6} \)\text{NEW PUB.seq:*} \\
4: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{VSO6} \)\text{PUBCOMB.seq:*} \\
5: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{VSO7} \)\text{NEW PUB.seq:*} \\
6: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{VSO8} \)\text{NEW PUB.seq:*} \\
6: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{VSO9} \)\text{PUBCOMB.seq:*} \\
6: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{USO9} \)\text{PUBCOMB.seq:*} \\
10: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{USO9} \)\text{PUBCOMB.seq:*} \\
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12: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{USO9} \)\text{PUBCOMB.seq:*} \\
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15: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{USO9} \)\text{PUBCOMB.seq:*} \\
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16: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{USO0} \\ \text{UBCOMB.seq:*} \\
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17: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{USO0} \\ \text{UBCOMB.seq:*} \\
18: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{UBCOMB.seq:*} \\
19: \( \cgn2_6 \)\text{ptodata} \( 1 \)\text{pubpna} \\ \text{UBCO
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	166	28.1	526	16	US-10-029-386-11178	Sequence 11178, A
	7.	•	2082	13	US-10-076-069-1	Sequence 1, Appli
	9	•	3179	19	US-10-840-455-20	Sequence 20, Appl
	9	•	25138	19	US-10-840-455-44	4
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	4	•	440	14	US-10-184-644-202	•
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equence 52, equence 10, equence 71,	equence 39087, equence 39088, equence 39087, equence 39088,	Sequence 27296, A Sequence 69519, A Sequence 3895, Ap Sequence 1, Appli Sequence 1, Appli
-52 -10 -10 -10 -10 -10 -10 -10 -10 -10 -10	-10-363-345A-39 -10-363-345A-39 -10-363-483A-39 -10-363-483A-39	US-10-437-963-27296 US-10-437-963-69519 US-10-156-761-3895 US-10-156-761-1 US-10-374-903A-1
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EST HUMAN HIT: BG720189.1, EVALUE 0
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NT HIT: gil6178011, EVALUE 0.00e+00
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Pred. No. 3e-161;
0; Mismatches
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Sequence 24898, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN; TITLE OF INVENTION: EXPRESSION ANALYSIS TWC; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine ve
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illarity 99.7%;
Conservative
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FEATURE:
OTHER INFORMATION: MAP
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LENGTH: 598
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                                             CTCCAGAATGAAGTGCCACCCCAGCCTGATCCAGTCTTCTTAGAAGCTCTGAGCTCCCGG
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; Sequence 6064, Application US/09867701
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6064
; LENGTH: 506
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Pred. No. 5.1e-130;
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ilarity 98.6%;
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Sequence 1239, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
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Pred. No. 1.5e-160;
2; Mismatches 0;
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Best Local Similarity 99.3%;
Matches 587; Conservative
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LOCATION: (57)...(57)
OTHER INFORMATION: n equals
0-106-698-1239
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LENGTH: 1596
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Sequence 1, Application US/10076069 Publication No. US20020177214A1 GENERAL INFORMATION:
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larity 55.0%;
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FEATURE:
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nes 166; Conser
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115; Conser
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FEATURE:
NAME/KEY: CDS
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LENGTH: 2082
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Best Local S
Matches 115
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US-09-867-701-6239

Sequence 6239, Application US/09867701

GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 186.6; DB 9;
Pred. No. 3.5e-45;
); Mismatches 4;
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Best Local Similarity 97.1%;
Matches 201; Conservative
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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.64
; OTHER INFORMATION: SWISSPROT HIT: Q60963, EVALUE 2.20e+00
; OTHER INFORMATION: NT HIT: gil5718683, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA426355.1, EVALUE 1.00e-114
US-10-029-386-11178
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Pred. No. 5.2e-39;
0; Mismatches 0;
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE E
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ. ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.;
SEQ ID NO 11178
LENGTH: 526
                                                                                         SINGLE
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Pred. No. 0.0009
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TITLE OF INVENTION: HEPP, A NOVEL GENE WITH A
FILE REFERENCE: 39532-176599
CURRENT APPLICATION NUMBER: US/10/076,069
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,923
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
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-10-069-386a

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Their Diagnostic and Therapeutic Use
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APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Edward V. Wancewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TE
FILE REFERENCE: ISPH-0527
CURRENT APPLICATION NUMBER: US/09/733,294A
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
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                        Telomerase Subunit, and 12 805C1
                                  TITLE OF INVENTION: Regulatory DNA Sequences
TITLE OF INVENTION: Telomerase Subunit, and
FILE REFERENCE: LeA 32 805C1
CURRENT APPLICATION NUMBER: US/10/840,455
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: PCT/EP98/08216
PRIOR APPLICATION NUMBER: US 09/582,246
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.2
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NUMBER OF SEQ ID NOS: 108
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-10-840-455-44
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Pred. No. 0.0019;
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APPLICANT: Hagen, Gustav
APPLICANT: Hagen, Gustav
APPLICANT: Wick, Maresa
APPLICANT: Wick, Maresa
APPLICANT: Zubov, Dmitry
TITLE OF INVENTION: Regulatory DNA Sequences of
TITLE OF INVENTION: Telomerase Subunit, and The
FILE REFERENCE: LeA 32 805C1
CURRENT APPLICATION NUMBER: US/10/840,455
CURRENT FILING DATE: 2004-05-06
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 1997-12-24
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Publication No. US20050032094A1
GENERAL INFORMATION:
APPLICANT: Bayer Aktiengesellschaf!
APPLICANT: Hagen, Gustav
APPLICANT: Wick, Maresa
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NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.2
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
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Pred. No. 0.0028;
); Mismatches 136;
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CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 202, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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                                                                                                                                                                                                                                                                                             ; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
US-09-733-294A-30
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin I
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
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                             NAME/KEY: intron
LOCATION: (42944)...
OTHER INFORMATION: INAME/KEY: exon
LOCATION: (46130)...
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Best Local Similarity
Matches 139; Conser
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NAME/KEY: exon
LOCATION: (47036)...
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NAME/KEY: intron
LOCATION: (47174).
LOCATION: (42882).
OTHER INFORMATION:
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                                                                                                                                    NAME/KEY: intron LOCATION: (46255)
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APPLICANT: Coddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Applicant SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLE;
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184, 634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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Pred. No. 0.0043;
L; Mismatches 169;
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                                       Score 44.8; DB 1
Pred. No. 0.0043;
                                                                Mismatches
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illarity 18.8%;
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US-10-184-634-202
Sapien
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; ORGANISM: Homo US-10-184-644-202
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Best Local S
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                                                 .. NAGC. N. NSTYBSCRC. . TBTC
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Sequence 52, Application US/10063685

Publication No. US20030180909A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Gedard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Watanabe, Colin K.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/063,685

CURRENT FILING DATE: 2002-05-08

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 52
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                                               SSSCNNNHCNSCSCSSCS.SCCCSNSSCCCSCS.
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US-10-063-685-52
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US-10-140-472-10/c
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                                                                                                                                                   LICANT: Gerritsen, Mary E.

LICANT: Goddard, Audrey
LICANT: Godowski, Paul J.

LICANT: Godowski, Paul J.

LICANT: Gurney, Austin L.

LICANT: Sherwood, Steven
LICANT: Smith, Victoria

LICANT: Smith, Victoria

LICANT: Stewart, Timothy A.

LICANT: Watanabe, Colin K

LICANT: Wood, William

LICANT: Wood, William

LICANT: Shang, Zemin

LE OF INVENTION: SECRETED AND TRANSMEMBRANE

LE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                      TRANSMEMBRANE
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CURRENT FILING DATE: 2002-04-15
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                         Sequence 10, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION:
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                                                                  Baker, Kevin P.
Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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Beresini, Maureen
DeForge, Laura
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
LENGTH: 594
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US-10-146-731-10/c
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CANT: Watanabe, Colin K
CANT: Wood, William
CANT: Zhang, Zemin
OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.8; DB
                                                                                                                                                                                                                                              TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15
Prior Application removed - See File Wrapper
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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larity 8.7%;
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Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy P
Gao, Wei-Qiang
Gerritsen, Mary E
                                                        Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                Smith, Victoria
Stewart, Timothy 7
Tumas, Daniel
                                        Goddard, Audrey
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
LENGTH: 594
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Best Local Similarity
Matches 28; Conser
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APPLICANT: Tumas, Danle,
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Towns, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
LENGTH: 594
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larity 8.7%; Pred. No. 0.0044;
Conservative 135; Mismatches 160;
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US-10-140-472-10
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tes/sec npda Search time 175 Seconds (without alignments) 573.529 Million cell up

US-10-069-386A-2 1033 1 MEGGLKRKHSDLEEEEERWE score Title: Perfect sc Sequence:

196

.. APGSWEWNELDHIMEIILGS

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residue 512079187 seds, 1612378 Searched

1612378 satisfying chosen parameters: hits of number Total

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UniProt_03:*
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Databas

a rinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

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Q96CQ2
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STD1 MOUSE
STD1 HUMAN
Q6P771
Q9DCZ2
STD2 MOUSE
Q6GM81
CCA4 MOUSE
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Q6GF1
Q9BQ18
Q7ZZ27
STD2 HUMAN
Q76M72
Q9BQ18
Q6DF1
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P85B HUMAN
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DB Length Query Match 1033 1026 871 217 217 217 217 213 140.5 1133 1133 1133 1105.5 1105.5 100 98 97 97.5 96 Score Result No.

Q64092 mus musculu	Q7tncl mus musculu	Q8cgdl mus musculu	Q8cfq8 mus musculu	Q8cft2 mus musculu	Q8pie4 xanthomonas	Q871u4 neurospora		human t	Q76qa3 human t-cel	human	Q82440 human t-cel	Q9dks2 human t-cel	Q9wi14 human t-cel
TFE3 MOUSE	Q7TNC1	Q8CGD1	Q8CFQ8	QBCFT2	Q8PIE4	Q871U4	070641	008833	Q76QA3	Q82343	Q82440	Q9DKS2	Q9W114
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TISSUE=Cvary, and Uterus;

X REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bross S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Boutfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human man and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Pred. No. 5.
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Submitted (APR-2003) to the EMB
EMBL; BC014061; AAH14061.1; -.
EMBL; BC050643; AAH50643.1; -.
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
SEQUENCE 196 AA; 21768 MW;
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              Homo sapiens (Human)
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                                                TaxID=9606;
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 Name=SERTAD3;
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Q9ERC3;
01-MAR-2001
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Mammary gland;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.

A Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length huma
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ datak
EMBL; AF317202; AAG30951.1; -.
EMBL; BC034886; AAH34886.1; -.
MGD; MGI:2180697; Sertad3.
InterPro; IPR009263; SERTA.
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
PROSITE; PS00152; ATPASE ALPHA BETA; UNKNOWN 1.
SEQUENCE 197 AA; 21934 MW; CFF6FA4C0A91D7E7 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 RBT1
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Pred. No. 4.5e-59
3; Mismatches 18
                                                                                                                                                                                                                                     Cho J.M., Alaoui-Jamali M.A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ
  trans-activator
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STRAIN=C57BL/6J; TISSUE=Embryo, and Small intestine;

STRAIN=C57BL/6J; TISSUE=Embryo, and Small intestine;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.

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Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

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Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescle G.

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka T., Wanlestedt C., Wang Y., Watanabe Y., Walls C., Wun Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

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Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Nahara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Satosi V.,

Yasunishi A., Yoshino W., Waterston R., Lander E.S., Rogers J.,

Nahara A., Hashizuwi Y.,
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                   regulator
(CDK4-binding
                                                                                                                                                                                                                                                                                                                                                                                                                               Hau S.-I., Yang C.M., Sim K.G., Hentscher L..., Versions, Bonventre J.V.;
"TRIP-Br: a novel family of PHD zinc finger- and bromodomain-interacting proteins that regulate the transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotat 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A., FUNCTION, AND INTERACTIONS.
21231173; PubMed=11331592; DOI=10.1093/emboj/20.9.2273;
7, Yang C.M., Sim K.G., Hentschel D.M., O'Leary E.,
                                                                                                                                                                                                                                                                                                                                               (DEC-1999) to the EMBL/GenBank/DDBJ databases
           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
SERTA domain-containing protein 1 (Transcriptional interacting with the PHD-bromodomain 1) (TRIP-Br1)
protein p34SEI1) (SEI-1).
Name=Sertad1; Synonyms=Sei1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                              Obtani N., Hara E.; "Cloning of mouse SEI-1 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20:2273-2285 (2001)
 Q9D888;
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commercial
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Acts at E2F-responsive promoters to integrate signals provided by PHD- and/or bromodomain-containing transcription factors. Stimulates E2F-1/DP-1 transcriptional activity. Renders the activity of cyclin D1/CDK4 resistant to the inhibitory effects of P16(INK4a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ELDEAELDYLMDVLVG
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--> K (in Ref. 2; AAK52829).
989ADF8299DE84C5 CRC64;
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                                                                                                                                                                                                                                                                                                        SUBUNIT: Interacts with the PHD-bromodomain of TIF1, and p300/CBP. Binds to DP1. Also interacts with CDK4 SIMILARITY: Belongs to the TRIP-Br family. SIMILARITY: Contains I SERTA domain.
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33; Mismatches 64;
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25136 MW;
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L; AF366400; AAK52829.1; -
L; AF366401; AAK52830.1; -
L; AK004022; BAB23130.1; -
L; AK008303; BAB25588.1; -
L; BC016077; AAH16077.1; -
L; MGI:1913438; Sertadl.
erPro; IPR009263; SERTA.
n; PF06031; SERTA; 1.
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ilarity 31.5%;
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Uterus;

X EXCUENCE FROM N.A., AND VARIANT THR-31.

TISSUE=Uterus;

X Extrausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Kahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Myhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Cheneration and initial analysis of more than 15,000 full-length human
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Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,

Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D.,

Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.,

"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department

of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).'

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Acts at E2F-responsive promoters to integrate signals provided by PHD- and/or bromodomain-containing transcription factors. Stimulates E2F-1/DP-1 transcriptional activity. Renders the activity of cyclin D1/CDK4 resistant to the inhibitory effectors.
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                                                                                                                                                                                                        SEQUENCE FROM N.A., AND INTERACTION WITH CDK4.
MEDLINE=20047903; PubMed=10580009; DOI=10.1101/gad.13.22.3027;
Sugimoto M., Nakamura T., Ohtani N., Hampson L., Hampson I.N.,
Shimamoto A., Furuichi Y., Okumura K., Niwa S., Taya Y., Hara E.,
"Regulation of CDK4 activity by a novel CDK4 binding protein,
p34SEII.";
                        regulator
(CDK4-binding
                                                                                                                                                                                                                                                                                                                                                                                                                      Hau S.-I., Yang C.M., Sim K.G., Hentschel D.M., O'Leary E.,
Bonventre J.V.;
"TRIP-Br: a novel family of PHD zinc finger- and bromodomain-
interacting proteins that regulate the transcriptional activity
E2F-1/DP-1.";
EMBO J. 20:2273-2285(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRIM28
                                                                                                                               Euteleostom
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., FUNCTION, AND INTERACTIONS.
MEDLINE=21231173; PubMed=11331592; DOI=10.1093/emboj/20.9.2273;
Hsu S.-I., Yang C.M., Sim K.G., Hentschel D.M., O'Leary E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Interacts with the PHD-bromodomain of TIF1, and p300/CBP. Binds to DP1. Also interacts with CDK4. SIMILARITY: Belongs to the TRIP-Br family. SIMILARITY: Contains 1 SERTA domain.
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
25-OCT-2004 (Rel. 45, Last annotation update)
SERTA domain-containing protein 1 (Transcriptional
interacting with the PHD-bromodomain 1) (TRIP-Br1)
protein p34SEI1) (SEI-1).
Name=SERTAD1; Synonyms=SEI1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                        Genes Dev. 13:3027-3033(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of p16 (INK4a)
                                                                                                                                                                    TaxID=9606;
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http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                ----LADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFE
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A ltschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.W.,
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Sciurognathi; Muridae; Murinae; Ra
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                                                                                                                            proliferation;
TAS.
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SERTA.
A -> T (in dbSNP:268687)
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on update)
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69;
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92F25EA328F155B1
                                                                                                                                                                                                                                                                                                  Score 213; DB 1;
Pred. No. 1.5e-08
; Mismatches 69
                                                                                                                                         GO; GO:0008284; P:positive regulation of cell GO; GO:0000079; P:regulation of CDK activity;
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Last annotation
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s requires a license agreement (
an email to license@isb-sib.ch)
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                                                                                                                                          GO; GO:0000079; ...
InterPro; IPR009263; SERIA.
Pfam; PF06031; SERTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                      24673 MW;
                                        EMBL; AF117959; AAF08349.1; -
EMBL; AF366402; AAK52831.1; -
EMBL; AY130860; AAM77800.1; -
EMBL; BC002670; AAH02670.1; -
Genew; HGNC:17932; SERTAD1.
H-INVDB; HIX0015136; -.
                                                                                                                                                                                                                                                                                                 20.6%;
illarity 32.6%;
Conservative 3
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                  Similarity 76; Conser
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entities requires
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5-JUL-2004
5-JUL-2004
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05-JUL-2
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 more than 15,000 full-length
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Mammalía; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
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                                                                                                                                                                                                                                                                                                             enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                               SPAGLQSYQQALLRISLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a full-length mouse cDNA collection."
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                                                                                                                                        236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN PANTOM CONSOrtium;
                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male kidney cDNA, RIKEN full-length e
library, clone:0610008D10 product:TRIP-BR1, full insert
Name=Sertad1;
Mus musculus (Mouse).
                                                                    databases
                                                                                                                                        Length
                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                   148 DDFFLDIDTSAVEKE---PARAPPEP-PHNLFCAPGSWEW--
          sequences.";
id. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                     Score 208; DB 2; 1
Pred. No. 3.7e-08;
33; Mismatches 67;
                                                                                                                     E8B7502E0473ED8B
                                                                                                                                                                                                                     PRAPSLRRHVLIHNTLOOLOAALRLAPAPALPPEPL-
                                                               2003) to the EMBL/GenBank/DDBJ
AAH61808.1; -.
9263; SERTA.
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 of
 analysis
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                                                                                                                                                          33;
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                                                                                                                     25419 MW;
                                                                                                                                        20.1%;
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                                                                           EMBL, BC061808, AAH61808.1
InterPro, IPR009263; SERTA
Pfam, PF06031; SERTA, 1.
Hypothetical protein.
SEQUENCE 236 AA; 25419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ional annotation of 409:685-690(2001).
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
 and initial
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The FANTOM Consortium,
                                                   Tissues
Strausberg R.;
Thmitted (NOV-2003)
                                                                                                                                                Similarity 76; Conser
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                                        Y.Z
                   Proc. Natl. Acad.
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                                                TISSUE=Prostate;
          CDNA
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01-JUN-2001
01-JUN-2001
 "Generation
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           mouse
                                                                                                                                       Query Match
Best Local S
Matches 76
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                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Kidney;

K MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format
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R., Ohno M.,
C., Sakai K.,
, Shiraki T.,
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Kato H.,
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STRAIN=C57BL/6J; TISSUE=Kidney;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H. Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Fur Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hor Hanagaki T., Hara A., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shir Sano H., Sasaki D., Shibata K., Shibata Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AK002324; BAB22013.1; -.

MGD; MGI:1913438; Sertadi.
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STRAIN=CS7BL/6J; TISSUE=Kidney;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.1451(Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
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SEQUENCE 244 AA; 26
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67; Conserv
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AC Q9JJG5; Q8C609; Q
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"A Month of M.D. Schein J.E., Jones S.J.M., Marra M.A.;

"A Month of M.D. Schein J.E., Jones S.J.M., Marra M.A.;

"A Month of M.D. Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
NCBI_TaxID=10090;
25-OCT-2004 (Rel. 45, Last annotation update,
SERTA domain-containing protein 2 (Transcriptional regulator
interacting with the PHD-bromodomain 2) (TRIP-Br2).
Name=Sertad2; Synonyms=Kiaa0127;
Mus musculus (Mouse).
                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.
Hashimoto K.;
"Isolation of full-length cDNA clones from mouse brain cDNA made by oligo-capping method.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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Proc. Natl. Acad. Sci. U.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                 O J. 20:2273-2285(2001).

FUNCTION: Acts at E2F-responsive promoters to integrate signal provided by PHD- and/or bromodomain-containing transcription factors (By similarity).

SIMILARITY: Belongs to the TRIP-Br family.

SIMILARITY: Contains 1 SERTA domain.
                                                                                of
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                                                       "TRIP-Br: a novel family of PHD zinc finger- and bromodomain interacting proteins that regulate the transcriptional active E2F-1/DP-1."; EMBO J. 20:2273-2285(2001).
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SEQUENCE OF 129-309 FROM N.A.
MEDLINE=21231173; PubMed=11331592; DOI=10.1093/emboj/20.
Hsu S.-I., Yang C.M., Sim K.G., Hentschel D.M., O'Leary
Bonventre J.V.;
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-> S (in Ref. 4).
-> A (in Ref. 1).
D4178688F0DF8F00 CRC64;
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Pred. No. 0.
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EMBL; AK076787; BAC36480.1;
EMBL; BC014726; AAH14726.1;
EMBL; AF366403; AAK52832.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%;
24.8%;
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27,
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InterPro; IPR009263; SERTA
Pfam; PF06031; SERTA; 1.
Transcription regulation.
CONFLICT 138 140
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Q6GM81;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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145
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MGD; MGI:1931026; Se
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77; Conserv
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145
234
309 AA;
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                                                                                                MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
A Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                     analysis of more than 15,000 full-length human
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                             Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleos!
Amphibía, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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 annotation update)
                                                                                                                                                                                                                                                                                                               sequences.";
id. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
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  Last
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Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the
 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC074195; AAH74195.1;
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
SEQUENCE 248 AA; 27319 M
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(TrEMBLrel.
                                                             Xenopus.
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           MGC82098 protein
Name=MGC82098;
                                                                      NCBI_TaxID=8355;
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Richardson P.;
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                                                             Xenopodinae;
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RESULT

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TISSUE=Breast tumor;

X TISSUE=Breast tumor;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rlakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=C57BL/6J; TISSUE=Mesonephros;

NRAIN=C57BL/6J; TISSUE=Mesonephros;

OKazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Gasterland T., Garibodi M., Gissi C., Godzik A., Gough J.,

A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurcchkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

A Konagaya A., Schneider C., Semple C.A., Setou M., Shimada K.,

Petrovsky N., Pillais R., Pontius J.U., Reid J., Ring B.Z., Ringwald M.,

Petrovsky N., Pillais R., Pontius J.U., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Nulming L.G., Wynshaw Boris A., Yanagisawa M., Yang I., Yang L.,

Vuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsun N.,

A Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakai K., Ishikawa T.,

Nataraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Nilming L.G., Wynshaw Boris A., Yanagisawa T., Fukuda S.,

A Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N., Sakai K., Sakai K., Ishikawa T., Koshino M., Waterston R., Lander E.S., Rogers J.,

Nature 420:563-573(2002).

I. Nature 420:563-573(2002).
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Q9CWMZ; Q921E8; Q99MP6;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cell division cycle associated protein 4 (Hematopoietic progenitor
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Bone marrow;
MEDLINE=21375891; PubMed=11482882; DOI=10.1006/bcmd.2001.0434;
Abdullah J.M., Jing X., Spassov D.S., Nachtman R.G., Jurecic R.;
"Cloning and characterization of Hepp, a novel gene expressed preferentially in hematopoietic progenitors and mature blood cell prod Cells Mol. Dis. 27:667-676(2001).
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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us-10-069-386a-2

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NCBI_TaxID=7955
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in
                                                                                                 TISSUE SPECIFICITY: Expressed preferentially in hematopoieti progenitors and mature blood cells. Expressed at low levels heart, lung, spleen, and thymus and at a higher level in mus DEVELOPMENTAL STAGE: Developmentally regulated. Preferential expression in both fetal and adult hematopoietic progenitors mature blood cells during embryonic and adult hematopoiesis. SIMILARITY: Belongs to the TRIP-Br family.
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL outhe European Bioinformatics Institute. There are no restricticuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.chor send an email to license@isb-sib.ch).
                                                 99:16899-16903(2002).
in molecular regulation of hematoge commitment and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinifo
                          full-lengt
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-> A (in Ref. 3).
52EC046EFDDF326E CRC64;
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smai
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 136; DB 1
Pred. No. 0.012;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                         IL; AK010535; BAB27012.2; -.
IL; AF322238; AAK31074.1; -.
IL; AK032980; BAC28109.1; -.
IL; BC012953; AAH12953.1; ALT_INIT.
); MGI:1919213; Cdca4.
erPro; IPR009263; SERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                          mouse cDNA sequences.";
:. Natl. Acad. Sci. U.S.A.
FUNCTION: May be involved
                                                                             stem cells and progenitor
                                                                                                                                                                                                                                                                                                                                                                                                                           26107 MW;
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26.1%;
                                      and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                   196
213
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Name=sertad2;
                                                                                          differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                             237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 63; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio.
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InterPro; len
fam; PF06031; SE
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05-JUL-2004
05-JUL-2004
05-JUL-2004
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Best Local
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Matches
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TISSUE=Kidney;

X REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Yillalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

I "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ARAPPEPPHNLFCAPGSWEWNELDHIMEII
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62 LEKRVLINNMLRRIQDELKQEGNLRPLFFPPSPPPDDPVDESFREPQPAFSVLSMVAPPI
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Strausberg R.;
Strausberg R.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC067135; AAH67135.1; -.
ZFIN; ZDB-GENE-030616-569; sertad2.
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.";
. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein SEQUENCE 361 AA;
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81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Matches
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                                             ler family 1
system Xag)
                                                                                                                                                                                                                                                                                                                       GPRAPS
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LEKRVLINNMLRRIQDELKQEGNLRPLFFPPSPPPDDPVDESFREPQPAFSVLSMVAPPI
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SQSPALSASSLTSPSSGLSNPAPLEACLTPASLLEEDNVSLCTSPSPLAPPAPTSRLSPS
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                                                                                                        Euteleostomi;
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                                                                             Name=sertad2; Synonyms=SI:zC101N13.8;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinifo
                                                                                                                                                                                                                                                                                                                       -SY---QQALLRISLDKVQRSL
                                                                                                                                                                                                                                                                                                 176;
        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
SI:zC101N13.8 (Novel protein similar to human solute carrier (Neuronal/epithelial high affinity glutamate transporter, sysmember 1 (SLC1A1)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulator
                                                                                                                                                                                                                                                                         Length 383;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                        Kimberley A.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AL772154; CAD61094.1; -.
ZFIN; ZDB-GENE-030616-569; sertad2.
InterPro; IPR009263; SERTA.
Pfam; PF06031; SERTA; 1.
SEQUENCE 383 AA; 40402 MW; 76514201CDFC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    -FLGEEDFSLSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
SERTA domain-containing protein 2 (Transcriptional interacting with the PHD-bromodomain 2) (TRIP-Br2).
Name=SERTAD2; Synonyms=KIAA0127;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                             71;
                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                        Score 133; DB 2
Pred. No. 0.037;
5; Mismatches '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSMDGTEPP
                                                                                                                                                                                                                                                                                                                       -SPAGLO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- PVFLE
                                                                                                                                                                                                                                                                                                                                                                                                                    -PEPL-
                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                      LRRHVLIHNTLQQLQAALR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QNEVPPQPD-
                                                                                                                                                                                                                                                                                                                       GLKRKHSDLEEEEERWEW--
                                                                                                                 Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                         12.9%; 22.3%;
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TIGSILRELD-
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                     Similarity
81; Conser
                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    APAPALP-
                                                                                                                                       TaxID=7955
        01-JUN-2003
01-JUN-2003
01-MAR-2004
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VGS
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15-JUL-1998
15-JUL-1998
05-JUL-2004
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                                                                                                                             Cyprinidae;
NCBI TaxID=
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --YQQALLRISLDKVQRSLGPRAPSLRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSTSTEAATAATDSVKGTSSEAGTQKLDGPQESRADDSKLMDSLPGNFEITTSTGFLTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 TLDDILFADIDTSMYDFDPCTSSSGTASKMAPVSADDLLKTLAPYSSQPVTPSQPFKMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLINNMLRRIQEELKQEGSLRPMFTPSSQPTTEPSDSYREAPPAFSHLASPSSHPCDLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALPPE---PLFLGEEDFSLSATIGSILRELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi; Murinae; Rattus
                                                              Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
"Prediction of the coding sequences of unidentified human genes. IV
The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
analysis of cDNA clones from human cell line KG-1.";
DNA Res. 2:167-174(1995).
-!- FUNCTION: Acts at E2F-responsive promoters to integrate signals
provided by PHD- and/or bromodomain-containing transcription
factors (By similarity).
-!- SIMILARITY: Belongs to the TRIP-Br family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .88
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Pred. No. 0.12;
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Mismatches
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PubMed=8590280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGGLKRKHSDLEEEERWEWSPAGLQS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D50917; BAA09476.2; ALT_INIT. Genew; HGNC:30784; SERTAD2. InterPro; IPR009263; SERTA. Pfo6031; SERTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O76M68
O76M68;
O76M68;
O5-JUL-2004 (TrEMBLrel. 27, Cres
O5-JUL-2004 (TrEMBLrel. 27, Las)
O5-JUL-2004 (TrEMBLrel. 27, Las)
SynArfGEF.
Name=sag;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Solentia; Solen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33896 MW;
                    MEDLINE=96127530; Pubmed=859(Nagase T., Seki N., Tanaka A., Prediction of the coding sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLDD-FFLDIDTSAVEKEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Inaba Y., Zhang J.P.,
Suzuki T.;
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les 71; Conser
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1082
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C TISSUE=Brain.

X MEDLINE=257929; PubMed=12693553;

A Nakajima D., Nagase T., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

A Nakajima D., Nagase T., Ohara O., Koga H.;

Nakajima D., Nagase T., Ohara O., Koga H.;

I. The complete nucleotide sequences of 400 mouse KIAA-homologous

II. The complete nucleotide sequences of 400 mouse KIAA-homologous

T randomly sampled from size-fractionated libraries.";

I. The complete nucleotide sequences of cDNA clones

T randomly sampled from size-fractionated libraries.";

EMBL; AKI22446; BAC65728.1; -.

RESSP; Q15438; 1BC9.

RGD; MGI:2677208; AKI22446.

InterPro; IPR001849; PH.

InterPro; IPR01849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:
|--DSCGSTPLRGPGSPVKVIHQPPLPPPPPPPYNHPHQFCPPGS 1179
                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LFCAPGS 180
                                                                                                                                                                                                                                                                                   -PAGLQSYQQALLRISLDKVQRSLGPRAP 50
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                                                                                                                                                                                                                                                                                                                                                   SATIGS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                    -APAPALPPEPLFLGEEDFSL
                                                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                    Length 1194;
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Supmitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB057643; BAD14305.1; -.
HSSP; Q15438; 1BC9.
InterPro; IPR000048; IQ_region.
InterPro; IPR000904; Sec7.
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on update)
                                                                                                                                                                                   4828FB1AA6F78B56
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                                                                                                                                                                                                                  Score 115; DB Pred. No. 3.6; 19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    ILRELDTSMDGTEPPONPVTPLGLQNEVPP-
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                                                                                           Pfam; PF00612; IQ; 1.
Pfam; PF01369; Sec7; 1.
SMART; SM00222; Sec7; 1.
PROSITE; PS50096; IQ; 1.
PROSITE; PS50190; SEC7; 1.
SEQUENCE 1194 AA; 129017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSSRYLGDSGLDDFFLDIDTSA-
                                                                                                                                                                                                                                                                                                                                                    SLRRHVLIHNTLQQLQAALRL-
                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                    5 LKRKHSDLEE-EEERWEWS--
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Name=AK122446; Synonyms=mKIA
                                                                                                                                                                                                               11.1%;
Similarity 24.3%;
58; Conservative 1
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SMART; SM00222; Sec7; 1.
PROSITE; PS50096; IQ; 1.
PROSITE; PS50190; SEC7; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1130 LSC-YASSSS-
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SEQUENCE
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Q80TJ8;
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Matches
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Length 911;

DB 2;

Score 113.5;

11.0%;

Query Match

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12;
                                                                                                                                              -----OPDPVFLEAL 137
                                                                                  98
                                                                                                                                                                               --VEKEPARAPPEPPHN---LFCAPGS 180
                                                                                                                                                                                                       896
                                                                                51 SLRRHVLIHNTLQQLQAALRL----APAPA-----LPPEPLFLGEEDFSLSATIGSI
                                                                                                          ---PSP
                                  ---PAGLOSYQQALLRISLDKVQRSLGPRAP
             Gaps
                                                                                                                                                                                              97;
            Indels
                                                                                                      754 ESSGEVSIHNRLÓTSÓHSPKKGVERGAÞAÞSPPTSPPPLÞPDPQ--
          62;
                                                                                                                                 99 LRELDTSMDGTEPPQNPVTPLGLQNEVPP----
Pred. No. 3.4; ); Mismatches
                                                                                                                                                                                138 SSRYLGDSGLDDFFLDIDTSA---
        19;
                                  5 LKRKHSDLEE-EEERWEWS--
Best Local Similarity 25.2%; Matches 60; Conservative
                                                                                                         <del>Q</del>
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Search completed: April 25, 2005, 12:32:29 Job time : 178 secs